```
OM protein - protein search, using sw model

                    GenCore version 4.5
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Run on:             May 7, 2002, 12:22:25 ; Search time 67.39 Seconds
                                           (without alignments)
                                           135.198 Million cell updates/sec

Title:              US-09-155-739-11
Perfect score:      655
Sequence:           1 QVQLVQSGAEVKKPGASVKV................NYGVYAMDYWGQGTLVTVSS 123

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched:           522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters:        522463

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :          A_Geneseq_1101:*
                    1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
                    2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	655	100.0	123	16	AAR81323	Humanized VLA-4 an
2	655	100.0	142	16	AAR81333	Human VLA-4 reshap
3	655	100.0	142	18	AAW22428	Humanised alpha-4
4	648	98.9	123	18	AAW22413	Humanised alpha-4 a
5	552	84.3	123	16	AAR81330	Mouse anti-VLA-4 a
6	544	83.1	140	16	AAR81327	Mouse VLA-4 antibo
7	544	83.1	140	18	AAW22410	Alpha-4 integrin m
8	523.5	79.9	120	19	AAW44124	Heavy chain variab
9	523.5	79.9	431	22	AAB30693	A fusion of single
10	523	79.8	136	16	AAR76681	Human/murine chime
11	523	79.8	136	17	AAW04396	Chimaeric human/mu

12	523	79.8	269	16	AAR76682	Human ONS-M21 anti
13	523	79.8	269	17	AAW04397	Chimaeric human/mu
14	515	78.6	119	16	AAR81325	Humanised VLA-4 an
15	515	78.6	119	18	AAW22426	Humanised alpha-4
16	512	78.2	119	16	AAR81324	Humanised alpha-4
17	512	78.2	119	18	AAW22425	Humanised alpha-4
18	507.5	77.5	135	21	AAR07969	A heavy chain vari
19	504.5	77.0	118	14	AAR37611	hIL2R Ab H chain v
20	503	76.8	119	20	AAY52717	Humanised ATR-5 H
21	503	76.8	119	22	AAB74978	Humanised ATR-5 H
22	499	76.2	119	22	AAY52719	Humanised ATR-5 H
23	499	76.2	136	17	AAB74980	Humanised antibod
24	495	75.7	119	16	AAR92084	Human 2*CL antibod
25	495	75.6	119	16	AAR81331	Humanised ATR-5 H
26	493	75.3	119	20	AAY52718	Humanised ATR-5 H
27	493	75.3	119	22	AAB74979	Humanised ATR-5 H
28	492	75.1	117	15	AAR57476	CDR-grafted anti-R
29	492	75.1	117	17	AAR92079	Murine 1308F VH CD
30	492	75.1	136	15	AAR57481	Humanised 1308F VH
31	491	75.0	119	17	AAY52708	Humanised ATR-5 H
32	491	75.0	119	22	AAB74969	Humanised ATR-5 H
33	489.5	74.7	120	18	AAW27551	Human Ab heavy cha
34	489	74.7	119	20	AAY52720	Humanised ATR-5 H
35	489	74.7	119	22	AAB74981	Humanised ATR-5 H
36	487.5	74.4	120	15	AAR74491	Humanised anti-CD1
37	487	74.4	119	20	AAY52712	Humanised ATR-5 H
38	487	74.4	119	20	AAY52715	Humanised ATR-5 H
39	487	74.4	119	22	AAB74973	Humanised ATR-5 H
40	487	74.4	119	22	AAB74976	Humanised ATR-5 H
41	486	74.2	140	18	AAW21847	Humanised heavy ch
42	486	74.2	143	15	AAR59942	Anti-VLA4 rAb huma
43	484.5	74.0	139	14	AAR33953	gH1 variable domai
44	484.5	74.0	139	18	AAW29753	CDR-grafted humani
45	484.0	74.0	139	21	AAY56877	gH1 variable domai

ALIGNMENTS

RESULT 1
AAR81323
AAR81323 standard; Protein; 123 AA.

ID   AAR81323 standard; Protein; 123 AA.
XX
AC   AAR81323;
XX
DT   02-APR-1996 (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 11; Page 69; 105pp; English.

```
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Ha, directed against leukocyte adhesion molecule VLA-4.
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ98892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence    123 AA;

Query Match     100.0%;  Score 655;  DB 16;  Length 123;
Best Local Similarity   100.0%;  Pred. No. 4e-53;
Matches  123;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
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Db    1  qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky  60

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt  120

Qy  121  VSS  123
         |||
Db  121  vss  123


RESULT 2
AAR81333
ID   AAR81333 standard; protein; 142 AA.
XX
AC   AAR81333;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Region          20..49
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /note= "framework region 3"
FT   Region          118..131
FT                   /note= "complementarity determining region 3"
FT   Region          132..142
FT                   /note= "framework region 4"
XX
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PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99894.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 11; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 heavy
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC   subcloned into mammalian cell expression vectors containing human
CC   kappa or gamma-1 constant regions.  In the humanized heavy chain,
CC   amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig H chain.  Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells.  The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as multiple
CC   sclerosis.  They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis.  The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence    142 AA;

Query Match     100.0%;  Score 655;  DB 16;  Length 142;
Best Local Similarity   100.0%;  Pred. No. 4.7e-53;
Matches  123;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   20  qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky  79

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
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Db   80  dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt  139

Qy  121  VSS  123
         |||
Db  140  vss  142
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```
RESULT 3
AAW22428
ID   AAW22428 standard; protein; 142 AA.
XX
AC   AAW22428;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
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SQ  Sequence  142 AA;

    Query Match  100.0%;  Score 655;  DB 18;  Length 142;
    Best Local Similarity  100.0%;  Pred. No. 4.7e-53;
    Matches 123;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
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Db   80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyyamdywgqgtlvt 139

Qy  121 VSS 123
        |||
Db  140 vss 142

RESULT  4

AAW22413
ID   AAW22413 standard; protein; 123 AA.
XX
AC   AAW22413;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VH Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
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FT   Region          1..30
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Misc-difference 27..30
FT                   /note= "21/28'CL residues 27-30 are replaced by
FT                   those of MAb 21.6, involved in antigen
FT                   binding"
FT   Region          31..35
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          36..49
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          67..98
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Misc-difference 72
FT                   /note= "21/28'CL Arg-72 is substd. by Ala of mouse
FT                   21.6 VL, important in supporting the CDR2
FT                   loop"
FT   Region          99..112
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          113..123
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
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```
KW   transplant rejection; graft versus host disease;
KW   atopic dermatitis; psoriasis; myocardial ischaemia; nephritis;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
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FT   Peptide         1..19
FT                   /label= Leader
FT   Protein         20..142
FT                   /label= Mat_protein
FT                   /note= "VH version Ha (Claim 25)"
FT   Region          20..49
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Region          50..55
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          55..67
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
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FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          86..117
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Region          118..131
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          132..142
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FT                   /note= "21/28'CL framework region 4"
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PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;  96WO-US18807.
XX
PR   21-NOV-1995;  95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74789.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 11; 107pp; English.
XX
CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22413).  It is composed of complementarity determining regions from
CC   the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human 21/28'CL framework.  It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences.  The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
```

XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
     asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 25; Fig 7; 107pp; English.
XX
CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VH
CC   region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human 21/28'CL framework. It can be expressed
CC   in mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
XX
SQ   Sequence 123 AA;

Query Match
Best Local Similarity   98.9%;   Score 648;   DB 18;   Length 123;
Matches 122;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;
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Db   1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Qy   121 VSS 123
         |||
Db   121 vss 123

RESULT   5
AAR81330
ID   AAR81330 standard; Protein; 123 AA.
XX
AC   AAR81330;
XX
DT   02-APR-1996 (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
     antibody engineering.
XX
OS   Mus musculus.
XX

FH   Key   Location/Qualifiers
FT   Region   1..30
FT   /label= FR1
FT   /note= "mouse heavy chain variable framework
FT   region 1"
FT   Region   31..35
FT   /label= CDR1
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 1"
FT   Region   36..49
FT   /label= FR2
FT   /note= "mouse heavy chain variable framework
FT   region 2"
FT   Region   50..66
FT   /label= CDR2
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 2"
FT   Region   67..98
FT   /label= FR3
FT   /note= "mouse heavy chain variable framework
FT   region 3"
FT   Region   99..112
FT   /label= CDR3
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 3"
FT   Region   113..123
FT   /label= FR4
FT   /note= "mouse heavy light chain variable framework
FT   region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
     leukocyte adhesion to endothelial cells, partic. for treating
     inflammatory disease.
XX
PS   Disclosure; Page 68; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ98895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanised antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence 123 AA;

Query Match   84.3%;   Score 552;   DB 16;   Length 123;

```
Best Local Similarity  82.9%;  Pred. No. 1.2e-43;
Matches 102;  Conservative 11;  Mismatches 10;  Indels  0;  Gaps  0;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
         :||| |||||| |||||||||||||||||||||||||||||||:|||||||||||||||
Db    1  evqlqgsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky  60

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
         |||||: ||||||||:|||: |||| |||||||||||||||||||||||||||||||  ||
Db   61  dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvvyamdywgggtsvt  120

Qy  121  VSS  123
          |||
Db  121  vss  123
```

```
RESULT  6
AAR81327
ID   AAR81327 standard; protein; 140 AA.
XX
AC   AAR81327;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FH
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Region          20..49
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /note= "framework region 3"
FT   Region          118..131
FT                   /note= "complementarity determining region 3"
FT   Region          132..140
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1994;  94US-0186269.
XX
PR   25-JAN-1995;  95WO-US01219.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99892.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 heavy chain variable
CC   region directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized heavy chain, amino acids H27,
CC   H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig H chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence  140 AA;
```

```
Query Match  83.1%;  Score 544;  DB 16;  Length 140;
Best Local Similarity  82.6%;  Pred. No. 7.5e-43;
Matches 100;  Conservative 11;  Mismatches 10;  Indels  0;  Gaps  0;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
         :||| |||||| |||||||||||||||||||||||||||||||:|||||||||||||||
Db   20  evqlqgsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky  79

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
         |||||: ||||||||:|||: |||| |||||||||||||||||||||||||||||||  ||
Db   80  dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvvyamdywgggtsvt  139

Qy  121  V  121
          |
Db  140  v  140
```

```
RESULT  7
AAW22410
ID   AAW22410 standard; protein; 140 AA.
XX
AC   AAW22410;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VH region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FH
FT   Peptide         1..19
FT                   /label= Leader
FT   Region          20..49
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /label= FR3
FT                   /note= "framework region 3"
```

FT   Region   118..131
FT   /label= CDR3
FT   Region   132..140
FT   /label= FR4
FT   /note= "complementarity determining region 3"
FT   /note= "framework region 4"
XX
PN   .WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74760.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 69-70; 107pp; English.
XX
CC   This polypeptide comprises the heavy chain variable region (VH) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC   complementarity determining regions (CDRs) of the 21.6 VH can be
CC   incorporated into a human 21/28'/CL framework to produce a claimed
CC   humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   140 AA;

Query Match   83.1%; Score 544; DB 18; Length 140;
Best Local Similarity 82.6%; Pred. No. 7.5e-43;
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy   1 QVQLVQSGAEVKRPGASVKVSCKASGFNIKDTYIHWYRQAPGQRLEWMGRIDPANGYTKY 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 evqlqgsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||| |||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   80 dpkfqgkatitadtssntaylqlsslsedtavyfcaregyygngnyyvyamdywgqgtsvt 139

RESULT 8

AAW44124

ID   AAW44124 standard; Protein; 120 AA.
XX
AC   AAW44124;
XX
DT   05-JUN-1998 .(first entry)
XX
DE   Heavy chain variable region of humanised NR-LU-13 antibody NRX451.

XX
KW   Heavy chain; variable region; murine; mouse; human; cancer antigen;
KW   antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
KW   treatment.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FH
FT   Region   31..35
FT   /note= "complementarity determining region 1"
FT   Region   50..59
FT   /note= "complementarity determining region 2"
FT   Region   99..109
FT   /note= "complementarity determining region 3"
XX
PN   WO9746589-A2.
XX
PD   11-DEC-1997.
XX
PF   06-JUN-1997;   97WO-US10074.
XX
PR   07-JUN-1996;   96US-0660362.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Graves SS, Henry AH, Hylarides MD, Mallet RW, Pedersen JT,
PI   Rees AR, Renoim, Searle SMJ;
XX
DR   WPI; 1998-042124/04.
XX
PT   Humanised antibody binds same human cancer antigen as antibody
PT   NR-LU-13 - useful for pre-targeting methods, conventional antibody
PT   therapy and immunodiagnosis
XX
PS   Example 1; Fig 4; 100pp; English.
XX
CC   A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
CC   humanised murine anti-human cancer antigen antibody (Ab) NR-LU-13,
CC   NRX451.
CC   hAb, specifically NRX451, or its conjugates can be used for the
CC   manufacture of a diagnostic or medicament for cancer diagnosis or
CC   treatment. The hAb has reduced immunogenicity and toxicity in
CC   humans, but retains the ability to bind the NR-LU-13 antigen.
XX
SQ   Sequence   120 AA;

Query Match   79.9%; Score 523.5; DB 19; Length 120;
Best Local Similarity 82.9%; Pred. No. 4.9e-41;
Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy   1 QVQLVQSGAEVKRPGASVKVSCKASGFNIKDTYIHWYRQAPGQRLEWMGRIDPANGYTKY 60
         |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1 qvqlvqsgaevkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntkc 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||||||||||||||||||||||||||||||||||||||||||| |:||||||||||
Db   61 dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl--tgtwsldywgqgtlvt 117

RESULT 9

AAB30693

ID   AAB30693 standard; Protein; 431 AA.
XX
AC   AAB30693;
XX
DT   02-APR-2001 (first entry)

Left column

```
XX
DE   A fusion of single chain antibody/streptavidin.
XX
KW   Streptavidin; tumour cell; cancer; adenocarcinoma;
KW   hematological malignancy; huNR-LU-10; EGP40; EPCAM.
XX
OS   Synthetic.
OS   Streptomyces avidinii.
OS   Homo sapiens.
XX
PN   WO200075333-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US15595.
XX
PR   07-JUN-1999; 99US-0137900.
PR   03-DEC-1999; 99US-0168976.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX
DR   WPI; 2001-091213/10.
DR   N-PSDB; AAC86562.
XX
PT   New vector constructs for expressing genomic streptavidin fusion
PT   proteins which are useful for targeting tumour cells associated with
PT   cancer, e.g. adenocarcinomas -
XX
PS   Example 1; Fig 10; 100pp; English.
XX
CC   The present sequence encodes a fusion of the single chain antibody
CC   huNR-LU-10 and streptavidin. The antibody binds the antigen EGP40 or
CC   EPCAM. The fusion protein is expressed using vectors of the invention.
CC   The specification describes vector constructs for expressing streptavidin
CC   fusion proteins. The vector comprises a first nucleic acid encoding
CC   streptavidin or its functional variant operatively linked to a promoter,
CC   and a cloning site for insertion of a second nucleic acid sequence
CC   encoding a polypeptide to be fused with streptavidin, interposed between
CC   the promoter and the first nucleic acid sequence. Alternatively, the
CC   vector construct comprises a first nucleic acid, operatively linked to a
CC   promoter, encoding a polypeptide to be fused with streptavidin, and a
CC   cloning site for insertion of a second nucleic acid encoding at least
CC   129 amino acids of streptavidin or its functional variant. The fusion
CC   proteins are useful for targeting tumour cells, particularly tumour cells
CC   associated with cancer, e.g. adenocarcinomas or hematological
CC   malignancies. The vector construct is useful for expressing of
CC   streptavidin fusion proteins. In particular, these are useful as tools
CC   for medical diagnostics and therapeutic purposes, e.g. for detecting the
CC   presence or absence of, or treating, a target site within a mammalian
CC   host.
XX
SQ   Sequence    431 AA;
```

```
Query Match             79.9%;  Score 523.5;  DB 22;  Length 431;
Best Local Similarity   82.9%;  Pred. No. 2e-40;
Matches 102;  Conservative 8;  Mismatches 10;  Indels 3;  Gaps 1;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntks 207

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYIAMDYWGQGTLVT 120
          ||||||||||||||:||||||||||||||||||||||||||:||||||||||||||||||
Db    208 dlsfggrvtitadtsintaymelsslrsddtavyycsrevl--tgtwsldywgqgtlvt 264

Qy    121 VSS 123
          |||
Db    265 vss 267
```

Right column

```
RESULT 10
AAR76681
ID   AAR76681 standard; Protein; 136 AA.
XX
AC   AAR76681;
XX
DT   17-JAN-1996  (first entry)
XX
DE   Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
XX
KW   Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
KW   medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FH
FT   Peptide        1..19
FT                  /label= sig_peptide
FT   Peptide        20..50
FT                  /label= FR 1
FT   Peptide        51..55
FT                  /label= CDR 1
FT   Peptide        56..59
FT                  /label= FR 2
FT   Peptide        70..86
FT                  /label= CDR 2
FT   Peptide        87..118
FT                  /label= FR 3
FT   Peptide        119..126
FT                  /label= CDR 3
FT   Peptide        127..136
FT                  /label= FR 4
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994; 94WO-JP01763.
XX
PR   19-NOV-1993; 93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T, Sato K, Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94539.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 26; Page 94; 120pp; Japanese.
XX
CC   AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-
CC   RVL-M21g(gamma)1. The antibody is reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence    136 AA;
```

```
Query Match             79.8%;  Score 523;  DB 16;  Length 136;
Best Local Similarity   83.7%;  Pred. No. 6.2e-41;
Matches 103;  Conservative 4;  Mismatches 10;  Indels 6;  Gaps 2;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db     20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqglewmgridpadgngtky 79

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYIAMDYWGQGTLVT 120
          |||||||||||||:|||||||||||||||:|||||||||||||||||||||||||||||||
Db     80 dpkfqgrvtitadtsintaymelsslrsedtafyfca-sayyvn----qdywgqgtttvt 133
```

Left column (RESULT 11)

```
Qy   121 VSS 123
         |||
Db   134 vss 136

RESULT 11
AAW04396
ID   AAW04396 standard; Protein; 136 AA.
XX
AC   AAW04396;
XX
DT   09-DEC-1996 (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT
FT   Peptide        1..19
FT                  /label= sig_peptide
FT   Peptide        20..136
FT                  /label= mat_peptide
FT   Region         50..54
FT                  /label= CDR_1
FT   Region         69..85
FT                  /label= CDR_2
FT   Region         118..125
FT                  /label= CDR_3
XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994.
XX
PR   18-OCT-1994; 94JP-0252166.
PR   19-NOV-1993; 93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38653.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 5; Pages 38-39; 45pp; Japanese.
XX
CC   The present sequence is a fragment of the chimaeric human/murine
CC   monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by
CC   combining light and heavy variable region DNA, from a murine
CC   anti-human myeloblastoma cell MAb, with human light and heavy
CC   constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols.. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   136 AA;

Query Match   79.8%; Score 523; DB 17; Length 136;
```

Right column (RESULT 12)

```
Qy   121 VSS 123
         |||
Db   134 vss 136

Best Local Similarity   83.7%;  Pred. No. 6.2e-41;
Matches 103; Conservative  4; Mismatches  10; Indels  6; Gaps  2;

Qy    1 QVQIVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||:|||||||||||||||||||||||||||||||||||||||| |||||||||
Db   20 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpangytky 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNGYGVYAMDYWGQGTLVT 120
        |||||||||| ||||||||| :|||||||||||| |||| |       ||| |||| ||
Db   80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyyn-----qdyvgggttvt 133

RESULT 12
AAR76682
ID   AAR76682 standard; Protein; 269 AA.
XX
AC   AAR76682;
XX
DT   18-JAN-1996 (first entry)
XX
DE   Human ONS-M21 antibody Fv fragment.
XX
KW   Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric protein;
KW   medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT
FT   Peptide        1..22
FT                  /label= sig_peptide
FT   Region         23..139
FT                  /note= "heavy variable region"
FT   Region         140..154
FT                  /note= "linker"
FT   Region         155..269
FT                  /note= "light variable region"
FT   Region         262..269
FT                  /note= "FLAG"
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994; 94WO-JP01763.
XX
PR   19-NOV-1993; 93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T, Sato K, Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94548.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 35; Pages 98-99; 120pp; Japanese.
XX
CC   AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the
CC   human antibody ONS-M21 Fv fragment. The plasmid was used in the
CC   construction of an expression vector, contg. cDNA encoding a
CC   human/murine chimeric antibody, reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence   269 AA;
```

```
Query Match             79.8%;  Score 523;  DB 16;  Length 269;
  Best Local Similarity  83.7%;  Pred. No. 1.3e-40;
  Matches 103;  Conservative  4;  Mismatches 10;  Indels  6;  Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||||:|||||||||||||||||||||||||||:||||||||||||::|| |||
Db   23 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapsgqglewmgridpadgntky 82

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
        ||||||||| | :|||||||||||||||||| |:|| |||  ||||||| || ||
Db   83 dpkfqgrvtitadestntaymelssirsedtafyfca-sayyvn----qdywgqgttvt 136

Qy  121 VSS 123
        |||
Db  137 vss 139
```

```
RESULT 13
AAW04397
ID   AAW04397 standard; Protein; 269 AA.
XX
AC   AAW04397;
XX
DT   09-DEC-1996  (first entry)
XX
DE   Chimeric human/murine MAb ONS-M21 scFv fragment.
XX
OS   Synthetic.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..22
FT                  /label= sig_peptide
FT   Region         23.139
FT                  /note= "heavy variable region"
FT   Peptide        140..154
FT                  /label= linker
FT   Region         155..261
FT                  /note= "light variable region"
FT   Peptide        262..269
FT                  /label= FLAG
XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994;  94JP-0285057.
XX
PR   18-OCT-1994;  94JP-0252166.
PR   19-NOV-1993;  93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38662.
XX
PS   Example 6; Pages 40-41; 45pp; Japanese.
XX
CC   The present sequence is a scFv fragment from the chimaeric
CC   human/murine monoclonal antibody (MAb) ONS-M21. The MAb was
CC   prepd. by combining light and heavy variable region DNA, from a
CC   murine anti-human myeloblastoma cell MAb, with human light and
CC   heavy constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence  269 AA;
```

```
Query Match             79.8%;  Score 523;  DB 17;  Length 269;
  Best Local Similarity  83.7%;  Pred. No. 1.3e-40;
  Matches 103;  Conservative  4;  Mismatches 10;  Indels  6;  Gaps  2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||||:|||||||||||||||||||||||||||:||||||||||||::|| |||
Db   23 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapsgqglewmgridpadgntky 82

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
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Qy  121 VSS 123
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Db  137 vss 139
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RESULT 14
AAR81325
ID   AAR81325 standard; Protein; 119 AA.
XX
AC   AAR81325;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
XX
OS   Mus musculus.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1994;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 13; Page 70; 105pp; English.
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Hc, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
```

```
CC   21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   119 AA;

Query Match             78.6%;  Score 515;  DB 16;  Length 119;
Best Local Similarity   82.9%;  Pred. No. 2.9e-40;
Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Qy         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGIYGNYGVYAMDYWGQGTLVT 120
              ||||||||||||||||||||||||||||||||||||| ||:|:           ||||||||
Db         61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116

Qy        121 VSS 123
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Db        117 vss 119
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RESULT 15
ID   AAW22426
ID   AAW22426 standard; Protein; 119 AA.
XX
AC   AAW22426;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VH Hc.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FH
FT   Region          1..30
FT                   /label= FR1
FT                   /note= "21.6 framework region 1"
FT   Misc-difference 27..30
FT                   /note= "21/28'CL residues 27-30 are replaced by
FT                   those of MAb 21.6, involved in antigen
FT                   binding"
FT   Region          31..35
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          36..49
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          67..98
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Misc-difference 72
FT                   /note= "21/28'CL Arg-72 is substd. by Ala of mouse
FT                   21.6 VL, important in supporting the CDR2
```

```
FT   Region          99..112
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT                   loop"
FT   Misc-difference 102
FT                   /note= "21/28'CL Tyr-102 is substd. by Phe of human
FT                   21/28'CL complementarity determining region 3"
FT   Region          113..123
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;  96WO-US18807.
XX
PR   21-NOV-1995;  95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 5; Fig 7; 107pp; English.
XX
CC   This polypeptide, designated Hc, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6.  It is
CC   composed of complementarity determining regions (CDRs) from the VH
CC   region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human 21/28'CL framework.  It contains an
CC   additional amino acid substitution (Tyr102Phe) in comparison to
CC   claimed humanised 21.6 VH version Ha (see AAW22412).  Humanised
CC   21.6 VH and VL regions are used to produce claimed humanised 21.6
CC   antibodies useful in the manufacture of a medicament for treating
CC   asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC   bowel disease, rheumatoid arthritis, transplant rejection, graft
CC   versus host disease, tumour metastasis, nephritis, atopic
CC   dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC   mediated lung injury.  The humanised antibodies have a half-life
CC   in the human circulation essentially equivalent to that of
CC   naturally occurring human antibodies.
XX
SQ   Sequence   119 AA;
```

```
Query Match             78.6%;  Score 515;  DB 18;  Length 119;
Best Local Similarity   82.9%;  Pred. No. 2.9e-40;
Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
              ||||||||||||||||||||||||||||||||||| :|||||||||||||||:| || |||
Db          1 qvqlvqsgaevkkpgasvkvsckasgfniksyanhwvrqapggqrlewmgwinagngntky 60

Qy         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGIYGNYGVYAMDYWGQGTLVT 120
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Db         61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116

Qy        121 VSS 123
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Db        117 vss 119
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Search completed: May  7, 2002, 12:22:26
Job time: 247 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:           May 7, 2002, 12:23:04 ; Search time 32.41 Seconds
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Title:
Perfect score:    655
Sequence:         1 QVOLVQSGAEVKKPGASVKV..........NYGVYAMDYWGQGTLVTVSS 123

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters:          212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
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           2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
           3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
           4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
           5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
           6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	655	100.0	123	2	US-08-561-521-11	Sequence 11, Appl
2	655	100.0	123	5	PCT-US99-01219-11	Sequence 11, Appl
3	655	100.0	142	2	US-08-561-521-17	Sequence 17, Appl
4	655	100.0	142	5	PCT-US95-01219-17	Sequence 17, Appl
5	552	84.3	123	2	US-08-561-521-9	Sequence 9, Appl
6	552	84.3	123	5	PCT-US99-01219-9	Sequence 9, Appl
7	544	83.1	140	2	US-08-561-521-4	Sequence 4, Appl
8	544	83.1	140	5	PCT-US95-01219-4	Sequence 4, Appl
9	523	79.8	117	4	US-08-646-265A-132	Sequence 132, App
10	523	79.8	136	4	US-08-646-265A-99	Sequence 99, Appl
11	523	79.8	269	4	US-08-646-265A-109	Sequence 109, App
12	515	78.6	119	2	US-08-561-521-13	Sequence 13, Appl
13	515	78.6	119	5	PCT-US95-01219-13	Sequence 13, Appl
14	512	78.2	119	2	US-08-561-521-12	Sequence 12, Appl
15	512	78.2	119	5	PCT-US95-01219-12	Sequence 12, Appl
16	505	77.1	125	2	US-08-561-521-44	Sequence 44, Appl
17	505	77.1	125	5	PCT-US95-01219-44	Sequence 44, Appl
18	495	75.6	119	2	US-08-561-521-10	Sequence 10, Appl
19	495	75.6	119	5	PCT-US95-01219-10	Sequence 10, Appl
20	492	75.1	117	2	US-08-290-592E-17	Sequence 17, Appl
21	492	75.1	117	5	PCT-US95-10053-14	Sequence 14, Appl
22	492	75.1	117	5	PCT-US96-09448-17	Sequence 17, Appl
23	491.5	75.0	118	2	US-09-025-769B-36	Sequence 36, Appl
24	489.5	74.7	120	4	US-09-025-769B-59	Sequence 59, Appl
25	489.5	74.7	120	5	US-08-836-561-63	Sequence 63, Appl
26	486	74.2	140	3	US-08-137-117D-112	Sequence 112, App
27	484.5	74.0	135	1		
28	484.5	74.0	135	2	US-08-436-717-112	Sequence 112, App
29	484.5	74.0	139	1	US-08-253-877C-19	Sequence 19, Appl
30	484.5	74.0	139	2	US-08-452-164A-19	Sequence 19, Appl
31	484.5	74.0	139	3	US-08-603-024-18	Sequence 18, Appl
32	481	73.4	121	2	US-08-202-047-23	Sequence 23, Appl
33	481	73.4	121	1	US-08-964-690-23	Sequence 23, Appl
33	474	72.4	140	3	US-08-836-561-74	Sequence 74, Appl
34	474	72.4	121	3	US-08-882-882-53	Sequence 53, Appl
35	473	72.2	123	2	US-08-483-389-53	Sequence 53, Appl
36	473	72.2	123	2	US-08-487-1113D-53	Sequence 53, Appl
37	473	72.2	123	2	US-08-473-503-53	Sequence 53, Appl
38	473	72.2	123	2	US-08-483-932-53	Sequence 53, Appl
39	473	72.2	123	3	US-08-720-420A-53	Sequence 53, Appl
40	473	72.2	123	2	US-08-714-017-53	Sequence 53, Appl
41	473	72.2	123	3	US-08-475-680-53	Sequence 53, Appl
42	473	72.2	123	3	US-08-482-882-86	Sequence 86, Appl
43	472	72.1	123	2	US-08-483-389-86	Sequence 86, Appl
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ALIGNMENTS

RESULT 1
US-08-561-521-11
Sequence 11, Application US/08561521
Patent No. 5840299
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GENERAL INFORMATION:
   APPLICANT: Bendig, Mary M.
   APPLICANT: Leger, Olivier J.
   APPLICANT: Saldanha, Jose
   APPLICANT: Jones, S. Tarran
   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
   TITLE OF INVENTION: Adhesion Molecule VLA-4
   NUMBER OF SEQUENCES: 45
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Townsend and Townsend Khourie and Crew
   STREET: One Market Plaza, Steuart Tower, Suite 2000
   CITY: San Francisco
   STATE: California
   COUNTRY: USA
   ZIP: 94105
   COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: Patentin Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/561,521
   FILING DATE:
   CLASSIFICATION: 424
   PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US/08/186,269A
   FILING DATE: 25-JAN-1994
   ATTORNEY/AGENT INFORMATION:
   NAME: Smith, William L.
   REGISTRATION NUMBER: 30,223
   REFERENCE/DOCKET NUMBER: 15270-14
   TELECOMMUNICATION INFORMATION:
   TELEPHONE: 415-543-9600
   TELEFAX: 415-543-5043
   INFORMATION FOR SEQ ID NO: 11:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 123 amino acids
   TYPE: amino acid
   STRANDEDNESS: single
   TOPOLOGY: linear
   MOLECULE TYPE: protein
US-08-561-521-11
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Query Match        100.0%;  Score 655;  DB 2;  Length 123;
Best Local Similarity   100.0%;  Pred. No. 1.7e-58;
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RESULT 2
PCT-US95-01219-11
; Sequence 11, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-11

Query Match   100.0%; Score 655; DB 5; Length 123;
Best Local Similarity   100.0%; Pred. No. 1.7e-58;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Db 121 VSS 123

RESULT 3
US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-17

Query Match   100.0%; Score 655; DB 2; Length 142;
Best Local Similarity   100.0%; Pred. No. 2e-58;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79
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Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Db   80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy 121 VSS 123
          |||
Db 140 VSS 142

RESULT 4
PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-17

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Query Match       100.0%;  Score 655; DB 5;  Length 142;
Best Local Similarity  100.0%;  Pred. No. 2e-58;
Matches 123;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
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Db   80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 139

Qy  121 VSS 123
         |||
Db  140 VSS 142
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RESULT 5
US-08-561-521-9
Sequence 9, Application US/08561521
Patent No. 5842299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-9

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Query Match       84.3%;  Score 552; DB 2;  Length 123;
Best Local Similarity  82.9%;  Pred. No. 3.3e-48;
Matches 102;  Conservative 11;  Mismatches 10;  Indels 0;  Gaps 0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         :|| |||||:|| |||||:|| ||||||||||||:|||||||||||:|||||||||||||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
         ||||| ||||||||:||||:|:||:||||||||||||||||||||||||||||||||||
Db   61 DPKFQGRATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYGNYGVYAMDYWGQGTSVT 120

Qy  121 VSS 123
         |||
Db  121 VSS 123
```

RESULT 6
PCT-US95-01219-9
Sequence 9, Application PCT/US9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US95-01219-9

Query Match
Best Local Similarity   84.3%;   Score 552; DB 5; Length 123;
Matches 102; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
Pred. No. 3.3e-48;

```
Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
        |||||: | ||||||||||||:|| |||||||||||| | |||:|||:|||||||||||||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY   60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGIYGNYGVYAMDYWGQGTLVT  120
        |||||| :|||||||::|||||:|||| ||||||||:|||| |||||||||||||||| ||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT  120

Qy  121 VSS  123
        |||
Db  121 VSS  123
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RESULT 7
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 424
; APPLICATION NUMBER: US/08/186,269A

; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-561-521-4

Query Match
Best Local Similarity   83.1%;   Score 544; DB 2; Length 140;
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
Pred. No. 2.4e-47;

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Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
        |||||: | ||||||||||||:|| |||||||||||| | |||:|||:|||||||||||||
Db   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY   79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGIYGNYGVYAMDYWGQGTLVT  120
        |||||| :|||||||::|||||:|||| ||||||||:|||| |||||||||||||||| ||
Db   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT  139

Qy  121 V  121
        |
Db  140 V  140
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RESULT 8
PCT-US95-01219-4
; Sequence 4, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

```
;   LENGTH:  140 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
PCT-US95-01219-4

Query Match     83.1%;  Score 544;  DB 5;  Length 140;
Best Local Similarity  82.6%;  Pred. No. 2.4e-47;
Matches 100;  Conservative 11;  Mismatches  10;  Indels  0;  Gaps  0;

Qy   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTK  79

Qy  61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
        |||||| ||||||||| |||| ||| ||||||||| |||||||||||||||||||||| ||
Db  80  DPKFQGRATITADTSSNTAYLQLSSLTSEDTAVIFCAREGYYGNYGVYYAMDYWGQGTSVT 139

Qy 121  V 121
        |
Db 140  V 140
```

```
RESULT   9
US-08-646-265A-132
; Sequence 132, Application US/0846265A
; Patent No. 6214973
;   GENERAL INFORMATION:
;     APPLICANT:  OHTOMO, Toshihiko
;     APPLICANT:  SATO, Koh
;     APPLICANT:  TSUCHIYA, Masayuki
;     TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;     TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;     NUMBER OF SEQUENCES:  132
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Patentin Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/646,265A
;       FILING DATE:  09-SEP-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/JP94/01763
;       FILING DATE:  19-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 5-291078
;       FILING DATE:  19-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WEGNER, Harold C.
;       REGISTRATION NUMBER:  25,258
;       REFERENCE/DOCKET NUMBER:  53466/184
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  90136
;   INFORMATION FOR SEQ ID NO:  132:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  117 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
US-08-646-265A-132
```

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Query Match     79.8%;  Score 523;  DB 4;  Length 117;
Best Local Similarity  83.7%;  Pred. No. 2.4e-45;
Matches 103;  Conservative  4;  Mismatches  10;  Indels  6;  Gaps  2;

Qy   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy  61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
        |||||||||||||||||||||||||||||||||||||: ||   |:|           || |||
Db  61  DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 114

Qy 121  VSS 123
        |||
Db 115  VSS 117
```

```
RESULT  10
US-08-646-265A-99
; Sequence 99, Application US/0846265A
; Patent No. 6214973
;   GENERAL INFORMATION:
;     APPLICANT:  OHTOMO, Toshihiko
;     APPLICANT:  SATO, Koh
;     APPLICANT:  TSUCHIYA, Masayuki
;     TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;     TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;     NUMBER OF SEQUENCES:  132
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Patentin Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/646,265A
;       FILING DATE:  09-SEP-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/JP94/01763
;       FILING DATE:  19-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 5-291078
;       FILING DATE:  19-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WEGNER, Harold C.
;       REGISTRATION NUMBER:  25,258
;       REFERENCE/DOCKET NUMBER:  53466/184
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  90136
;   INFORMATION FOR SEQ ID NO:  99:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  136 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
US-08-646-265A-99
```

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Query Match     79.8%;  Score 523;  DB 4;  Length 117;
Best Local Similarity  83.7%;  Pred. No. 2.9e-45;
Matches 103;  Conservative  4;  Mismatches  10;  Indels  6;  Gaps  2;

Qy   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db    20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGGGTLVT 79
         ||||||||||||||||||||||||||||||||||||||||||||:||| |||
Qy    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||||||||||:|:|||||||||||||||||||||||:||| |||
Db    80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN----QDYWGQGTTVT 133
Qy   121 VSS 123
         |||
Db   134 VSS 136
```

RESULT 11
US-08-646-265A-109
; Sequence 109, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 5466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 90436
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-265A-109

Query Match   79.8%; Score 523; DB 4; Length 269;
Best Local Similarity   83.7%; Pred. No. 6.5e-45;
Matches 103; Conservative   4; Mismatches   10; Indels   6; Gaps   2;

```
Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||| ||||||||||||||||:|||||||||||||||||||||| |||
Db   23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        ||||||||||||:|:|||||||||||||||||||||||:||| |||
Db   83 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN----QDYWGQGTTVT 136
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```
Qy   121 VSS 123
         |||
Db   137 VSS 139
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RESULT 12
US-08-561-521-13
; Sequence 13, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-13

Query Match   78.6%; Score 515; DB 2; Length 119;
Best Local Similarity   82.9%; Pred. No. 1.6e-44;
Matches 102; Conservative   5; Mismatches 12; Indels   4; Gaps 1;

```
Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||:||||||||||||||||:||||||||||||| |:|||||| |||
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        |||||||||||:||||||||||||||||||||||||:||  |:  ||||||||||||||
Db   61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT 116
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RESULT 13
PCT-US95-01219-13

; Sequence 13, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein

PCT-US95-01219-13

Query Match   78.6%; Score 515; DB 5; Length 119;
Best Local Similarity   82.9%;   Pred. No. 1.6e-44;
Matches 102; Conservative   5; Mismatches 12; Indels   4; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTRY 60
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTRY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||||||||||||||||||||||||||||||||||||||||||| || ||||||||||
Db   61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS---GSNYWGQGTLVT 116

Qy 121 VSS 123
          |||
Db 117 VSS 119

RESULT 14
US-08-561-521-12
; Sequence 12, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4

; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein

US-08-561-521-12

Query Match   78.2%; Score 512; DB 2; Length 119;
Best Local Similarity   82.9%;   Pred. No. 3.1e-44;
Matches 102; Conservative   4; Mismatches 13; Indels   4; Gaps   1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| ||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||||||||||||||||||||||||||| || || ||||||||||||||
Db   61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS---GSNYWGQGTLVT 116

Qy 121 VSS 123
          |||
Db 117 VSS 119

RESULT 15
PCT-US95-01219-12
; Sequence 12, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
; COMPUTER READABLE FORM:

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;    MEDIUM TYPE: Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  Patentin Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  PCT/US95/01219
;    FILING DATE:  25-JAN-1995
;    CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/186,269
;    FILING DATE:  25-JAN-1994
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Smith, William L.
;    REGISTRATION NUMBER:  30,223
;    REFERENCE/DOCKET NUMBER:  15270-14
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  415-543-9600
;    TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH:  119 amino acids
;    TYPE:  amino acid
;    STRANDEDNESS:  single
;    TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-12
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Query Match            78.2%;    Score 512;    DB 5;    Length 119;
Best Local Similarity  82.9%;    Pred. No. 3.1e-44;
Matches  102;  Conservative   4;  Mismatches  13;  Indels   4;  Gaps    1;

Qy     1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPQRLEWMGRIDPANGYTKY  60
          |||||||||||||||||||||||||||||||||| :|||||||||||: |||||| |||
Db     1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQGLEWMGWINAGNGNTKY  60

Qy    61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
          ||||||||||||||||||||||||||||||| ||||| :|||||||||||
Db    61  SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYYGS---GSNYWGQGTLVT  116

Qy   121  VSS  123
          |||
Db   117  VSS  119
```

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Search completed: May  7, 2002, 12:23:04
Job time: 175 sec
```

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:47 ; Search time 37.68 Seconds
                 (without alignments)
                 248.659 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Title:
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKPGASVKV...........NYGVYAMDYWGQGTLVTVSS 123

Scoring table: US-09-155-739-11

                 BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   PIR_68:*
                 1:   pir1:*
                 2:   pir2:*
                 3:   pir3:*
                 4:   pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488.5	74.6	178	2	S29594	Ig gamma chain (WM
2	477	72.8	120	2	S03471	Ig heavy chain V-D
3	473.5	72.3	118	2	S36265	Ig heavy chain V-1
4	468	71.5	123	2	D33548	Ig heavy chain V-D
5	467	71.3	142	2	A32483	Ig heavy chain V r
6	465	71.0	122	2	S17586	Ig heavy chain V r
7	459.5	70.2	122	2	S06823	Ig heavy chain V r
8	456.5	69.7	132	2	PH0954	Ig gamma chain V r
9	455	69.5	116	2	S24289	Ig gamma-1 chain -
10	455	69.5	221	2	S49220	Ig heavy chain V r
11	450	68.7	129	2	S46393	Ig heavy chain V-D
12	449	68.5	115	2	S03482	Ig heavy chain V-D
13	447.5	68.3	135	2	S49530	anti-Sm antibody V
14	447	68.2	120	2	S03484	Ig heavy chain V-D
15	446.5	68.2	136	2	PH0960	Ig heavy chain V r
16	444	67.8	136	2	S04576	Ig heavy chain pre
17	443	67.6	119	2	PH0961	Ig heavy chain V r
18	441	67.4	268	2	A56446	Ig heavy chain V r
19	439.5	67.1	104	2	PH1665	Ig heavy chain V r
20	439.5	67.1	114	4	A47271	nitrophenyl phosph
21	439	67.0	133	2	C33548	Ig heavy chain V-1
22	439	67.0	627	2	S14683	Ig mu chain precur
23	438.5	66.9	114	2	PH1666	Ig heavy chain V r
24	438.5	66.9	118	2	PH1667	Ig heavy chain V r
25	437.5	66.8	137	2	S52445	Ig heavy chain V r
26	436.5	66.6	120	2	S31999	Ig heavy chain V r
27	435.5	66.5	120	2	PH0962	Ig heavy chain V r
28	435.5	66.5	128	2	PH0952	Ig heavy chain V r
29	433.5	66.2	126	2	B33548	Ig heavy chain V-1
30	433	66.1	127	2	PH0955	Ig heavy chain V r
31	433	66.1	135	2	PH0953	Ig heavy chain V r
32	431	65.8	126	2	I44151	Ig heavy chain V r
33	429.5	65.6	108	2	PH1012	Ig heavy chain V r
34	429	65.5	125	2	PH0957	Ig heavy chain V r
35	427.5	65.3	143	1	E1HUND	Ig heavy chain pre
36	427	65.2	125	2	S68170	Ig heavy chain V-1
37	427	65.2	125	2	A33548	Ig heavy chain V-1
38	426	65.0	127	2	S34014	Ig heavy chain V r
39	425	64.9	129	2	S36260	Ig heavy chain V r
40	424.5	64.8	147	2	PH1561	Ig gamma chain - m
41	424.5	64.8	171	2	S23623	Ig heavy chain V r
42	421	64.3	246	2	S38950	Ig gamma-2a chain
43	421	64.3	446	2	S40295	Ig heavy chain V r
44	420.5	64.2	122	2	PH1426	Ig heavy chain V r
45	420	64.1	121	2	S20783	Ig heavy chain V-1

ALIGNMENTS

RESULT   1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match   74.6%;   Score 488.5;   DB 2;   Length 178;
Best Local Similarity   75.6%;   Pred. No. 9e-37;
Matches   93;   Conservative 11;   Mismatches 14;   Indels 5;   Gaps 2;

Qy   1 QVQLVQSGAEVKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :|||:||||||.|||:.||| ||||||||||||||||||||:|||||||||||||||:|
Db   14 EVQLVQSGAELVKPGASVKLSCTASGFNIKDIYMHWVKQRPKQGLEWIGRIDPANGYTEY 73

Qy   61 DPKFQGRVTITADTSASTAYMEL.SSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||| ||||:|||||||||||| |||||||||||||| ||||||||||||||||||||
Db   74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG---GNY-AYGMDYWGQGTSVT 128

RESULT   2
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Molnier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982

Qy   121 VSS 123
           |||
Db   129 VSS 131

A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

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Query Match       72.8%;  Score 477;  DB 2;  Length 120;
Best Local Similarity  75.6%;  Pred. No. 6.3e-36;
Matches   93;  Conservative  11;  Mismatches  15;  Indels   4;  Gaps   1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :||| |||||:|| |||||||||:|||||||||||||:|| |||::|| ||||::|| |
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||||||||||:|||::|||||||||| |||| | |||||||||:::||| ||||||||| |
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR----GWLRDAMDYWGQGTISVT 116

Qy  121 VSS 123
         |||
Db  117 VSS 119
```

RESULT 3
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
R;Accession: S36265
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36265; MUID:93178448
A;Accession: S36265
A;Molecule type: mRNA
A;Status: preliminary; nucleic acid sequence not shown
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g999900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

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Query Match       72.3%;  Score 473.5;  DB 2;  Length 118;
Best Local Similarity  76.2%;  Pred. No. 1.3e-35;
Matches   96;  Conservative   6;  Mismatches  13;  Indels  11;  Gaps   2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||||||||||||| :||||||||||||||||||| ||||| :|| |
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGT 117
          |||||||||| |||||||||||||||||||||||||||: |
Db   61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGY------LDYWGQGT 112

Qy  118 LVTVSS 123
         ||||||
Db  113 LVTVSS 118
```

RESULT 4
D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
R;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr

RESULT 5
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
R;Accession: A32483
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
A;Reference number: A32483; MUID:89273586
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

```
Query Match       71.5%;  Score 468;  DB 2;  Length 142;
Best Local Similarity  74.8%;  Pred. No. 4.1e-35;
Matches   92;  Conservative   7;  Mismatches  24;  Indels   0;  Gaps   0;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||||||| :|||| :|:||:|||||||| |||||| :||:|:|| |
Db    1 QVQLVQSGAEVKKPGASVKVSCEASGYTFTGYHMHWVRQAPGQGLEWMGWINPSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGTLVT 120
          ||||||||| ||| :||||||| ||| || ||||| | |
Db   61 AEKFQGRVTITRDTSINTAYMELSRLRSDDTAVYYCARASYCGYDCYYFDYWGQGTLVT 120

Qy  121 VSS 123
         |||
Db  121 VSS 123
```

RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R;Accession: S17586
A;Title: Biochemical Implications from the variable gene sequences of an anti-cytochr
J. Mol. Biol. 221, 455-462, 1991
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.

```
Query Match       71.3%;  Score 467;  DB 2;  Length 123;
Best Local Similarity  73.2%;  Pred. No. 5.9e-35;
Matches    8;  Mismatches  22;  Indels   4;  Gaps   1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||| :|:|: ||||||||| |||||| :||:|::||
Db   11 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSGNSTNY 70

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE----GYYGNVGVYAMDYWGQG 116
          ||||||||| | |||:|||||||||||||||||||||:     :
Db   71 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130

Qy  117 TLVTVSS 123
         |||||||
Db  131 TLVTVSS 137
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forms.

A;Reference number: S17586; MUID:92015240
A;Accession: S17586
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match        71.0%;      Score 465;   DB 2;   Length 117;
Best Local Similarity   72.6%;   Pred. No. 7.3e-35;
Matches    90;  Conservative   15;  Mismatches  11;  Indels  8;  Gaps  3;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||| |||||| |||||||||||||||||||||||: ||||||||| :|||||||||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEGGLEWIGRIDPASGNTKY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGQGTLV 119
          |||||  || |||: :|||||| ||||||||||||||| : |||:|   ||||||||||
Db   61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113

Qy  120 TVSS 123
          ||||
Db  114 TVSS 117
```

RESULT 7
S06823
Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06823
A;Status: not compared with conceptual translation
A;Accession: S06815; MUID:90064531
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

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Query Match        70.2%;      Score 459.5;   DB 2;   Length 122;
Best Local Similarity   73.4%;   Pred. No. 2.4e-34;
Matches    91;  Conservative   13;  Mismatches  17;  Indels  3;  Gaps  3;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIH-WVRQAPGQRLEWMGRIDPANGYTK 59
          ||||| |||||| |||||||||||||||||||||| |||||||||| :|||||||||||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEGGLEWIGRIDPANGNTK 60

Qy   60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLV 119
          ||||||  || |||: :|||||| ||||||||||||||| ||| : |||||||||||||
Db   61 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR-GWL-RRDAMGVDYWGQGTSV 118

Qy  120 TVSS 123
          ||||
Db  119 TVSS 122
```

RESULT 8
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992

A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0954
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3

```
Query Match        69.7%;      Score 456.5;   DB 2;   Length 132;
Best Local Similarity   72.0%;   Pred. No. 4.8e-34;
Matches    95;  Conservative   1;  Mismatches  27;  Indels  9;  Gaps  1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||:||||||||||   :  ||:||||||||| |||||| ::    ||
Db    1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR--------EGYYGNYGVYAMD 111
          :|||||||||||| ||:|||||||||||||||||||||        |||:  ||  |||
Db   61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNYYYYGMD 120

Qy  112 YWGQGTLVTVSS 123
          :|||||:|||||
Db  121 VWGQGTTVTVSS 132
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RESULT 9
S24289
Ig gamma chain V region (J334/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Monchamont, B.
R;Description: Cloning and sequencing of the cDNA coding for the variable regions of
submitted to the EMBL Data Library, September 1991
A;Reference number: S24289
A;Status: preliminary
A;Accession: S24287
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

```
Query Match        69.5%;      Score 455;   DB 2;   Length 116;
Best Local Similarity   71.5%;   Pred. No. 5.7e-34;
Matches    88;  Conservative   13;  Mismatches  14;  Indels  8;  Gaps  2;

Qy    2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
          ||| :|||| ||||||||||||||:|||:|||:|||||: || |||||||||||||| :|
Db    1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60

Qy   62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
          |||||  || |||: :|||||| ||||||||||||||  |||      |||||||||| |
Db   61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARNAGYY-----FDYWGQGTLT 113

Qy  121 VSS 123
          |||
Db  114 VSS 116
```

RESULT 10
S49220

```
      Ig gamma-1 chain - mouse (fragment)
   C;Species: Mus musculus (house mouse)
   C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
   R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
   A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
   submitted to the EMBL Data Library, September 1994
   A;Reference number: S49220
   A;Accession: S49220
   A;Molecule type: mRNA
   A;Residues: 1-221 <KIP>
   A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:g541732.1; PID:g541779
   A;Experimental source: strain Balb/c
   A;Superfamily: immunoglobulin C region; immunoglobulin homology
   F;1-120/Domain: V region #status predicted <VRG>
   F;121-221/Domain: C region #status predicted <CRG>
   F;139-203/Domain: immunoglobulin homology <IMM>

   Query Match    69.5%;   Score 455;  DB 2;  Length 221;
   Best Local Similarity    70.7%;  Pred. No. 1.1e-33;
   Matches    87;  Conservative   12;  Mismatches   20;  Indels   4;  Gaps   1;

Qy   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
        |||||||||||||||||||||||||||| ||:||:|||||||||||||||||||| |||
Db   1  QVRLLESGAELVKSGASVKLSCTASGFNIKDTYIMHWVKQRPEQGLEWIGRIDPANGEIKY  60

Qy  61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGIYGNYGVYAMDYWGQGTLVT  120
        |||||| ||| |||:|||||||:||||||||||| ||:::| |     |||||| ||  |
Db  61  DPKFQGTATITADISTNTAVLQLSSLTSEDTAVVYCVRRG----YGSSQEPYWGQTTLT  116

Qy  121 VSS  123
         |||
Db  117 VSS  119


RESULT 11
S46393
      Ig heavy chain V region - human
   C;Species: Homo sapiens (man)
   C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
   R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
   A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
   J. Mol. Biol. 239, 68-78, 1994
   A;Reference number: S46390; MUID:94254092
   A;Accession: S46393
   A;Status: preliminary
   A;Molecule type: DNA
   A;Residues: 1-129 <FIG>
   A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
   A;Superfamily: immunoglobulin V region; immunoglobulin homology
   F;15-98/Domain: immunoglobulin homology <IMM>

   Query Match    68.7%;   Score 450;  DB 2;  Length 129;
   Best Local Similarity    70.5%;  Pred. No. 1.8e-33;
   Matches    91;  Conservative   10;  Mismatches   22;  Indels   6;  Gaps   2;

Qy   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
        ||||||||||||||||||||||||||||:
Db   1  QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY  60

Qy  61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG  114
        |||||||||||||||||||||| |||:|||||| |:|     || | |      ||||
Db  61  AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYYSANYYMDVWG  120

Qy  115 QGTLVTVSS  123
        |: |||| ||
Db  121 KGTTVTVSS  129


RESULT 12
S03482
      Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
   C;Species: Mus musculus (house mouse)
   A;Variety: strain BALB/c
   C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
   C;Accession: S03482; S07453
   R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
   EMBO J. 2, 867-872, 1983
   A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
   hypervariable regions.
   A;Reference number: S03471; MUID:8405768
   A;Accession: S03482
   A;Status: Preliminary
   A;Molecule type: mRNA
   A;Residues: 10-115 <ROC1>
   A;Cross-references: EMBL:X03219
   A;Note: this sequence was determined from the differentiated gene
   R;Rocca-Serra, J.; Mazie, J.C.; Molnier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
   J. Immunol. 129, 2554-2558, 1982
   A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
   A;Reference number: S07453; MUID:83058021
   A;Accession: S07453
   A;Status: preliminary
   A;Molecule type: protein
   A;Residues: 1-43 <ROC2>
   A;Superfamily: immunoglobulin V region; immunoglobulin homology
   F;15-98/Domain: immunoglobulin homology <IMM>

   Query Match    68.5%;   Score 449;  DB 2;  Length 115;
   Best Local Similarity    70.2%;  Pred. No. 1.9e-33;
   Matches    85;  Conservative   12;  Mismatches   18;  Indels   6;  Gaps   1;

Qy   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
        :||| |||||:|| |||||||||||||:|| ||||||||||||||:|||||| || |
Db   1  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIMHWVKQRPEQGLEWIGRIDPAKGNTKY  60

Qy  61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGIYGNYGVYAMDYWGQGTLVT  120
        |||||: ||| |||:|||||:|||||||||||||| ||:::| |     |||||| ||
Db  61  DPKFQGKATITDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR-----DYWGQGTTLT  114

Qy  121 V  121
        |
Db  115 V  115


RESULT 13
S49530
      anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
   C;Species: Homo sapiens (man)
   C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
   C;Accession: S49530
   R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
   submitted to the EMBL Data Library, October 1994
   A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
   A;Reference number: S48797
   A;Accession: S49530
   A;Status: preliminary
   A;Molecule type: mRNA
   A;Residues: 1-135 <MAH>
   A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
   A;Superfamily: immunoglobulin V region; immunoglobulin homology
   F;34-117/Domain: immunoglobulin homology <IMM>

   Query Match    68.3%;   Score 447.5;  DB 2;  Length 135;
   Best Local Similarity    72.8%;  Pred. No. 3.1e-33;
   Matches    91;  Conservative   7;  Mismatches   16;  Indels   11;  Gaps   2;

Qy   1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
        |||||||||||||||||||||||||||||||:|| |||||||||||||||| |:| | |
```

```
Db        20  QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY   79

Qy        61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYC--AREGYYGNYGVYAMDYWGQGTL  118
              :||| ||||||||:|:| ||||||| ||||||||||   |||
Db        80  AQKFQGRVTMFRDTSISTAYMELSRLRSDDTAVYYCARARTGY----------NYWGQGTL  130

Qy       119  VTVSS  123
              |||||
Db       131  VTVSS  135
```

```
RESULT    14

S03484

Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03471; MUID:8405768
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Mohier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
A;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology

Query Match             68.2%;  Score 447;  DB 2;  Length 120;
Best Local Similarity   71.5%;  Pred. No. 3e-33;
Matches  88;  Conservative  11;  Mismatches  20;  Indels  4;  Gaps  1;

Qy         1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQGRLEWMGRIDPANGYTKY  60
              :|||||||||||||||||||||:||||||:|||||||||:|:|:||||||||||      :|
Db         1  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANXNSKY  60

Qy        61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
              ||||||:|||||||:|:|||||||||||||||||| |||||||||
Db        61  GPKFQGXATITADTSSSAAYLQLSSLTSGDTAVYYCTR---------GWFRRDAMDYWGQGTSVT  116
```

```
Qy       121  VSS  123
              |||
Db       117  VSS  119
```

```
RESULT    15

PH0960

Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:9202880
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
```

```
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-124/Region: complementarity-determining 3

Query Match             68.2%;  Score 446.5;  DB 2;  Length 136;
Best Local Similarity   69.1%;  Pred. No. 3.8e-33;
Matches  94;  Conservative  1;  Mismatches  28;  Indels  13;  Gaps  1;

Qy         1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQGRLEWMGRIDPANGYTKY  60
              :|||||||||||||||||||:||  | ||||||:||||||:|:|:||||||||||
Db         1  QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY  60

Qy        61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-----------EGYYGNYGV  107
              |||||||:||||||:|:||||||||||||||||||||           ||   |
Db        61  AQKFQGRVTIIADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY  120

Qy       108  YAMDYWGQGTLVTVSS  123
              | || ||||||| |||||
Db       121  YGMDVWGQGTTVTVSS  136
```

```
Search completed: May  7, 2002, 12:23:48
Job time: 199 sec
```

```
OM protein - protein search, using sw model
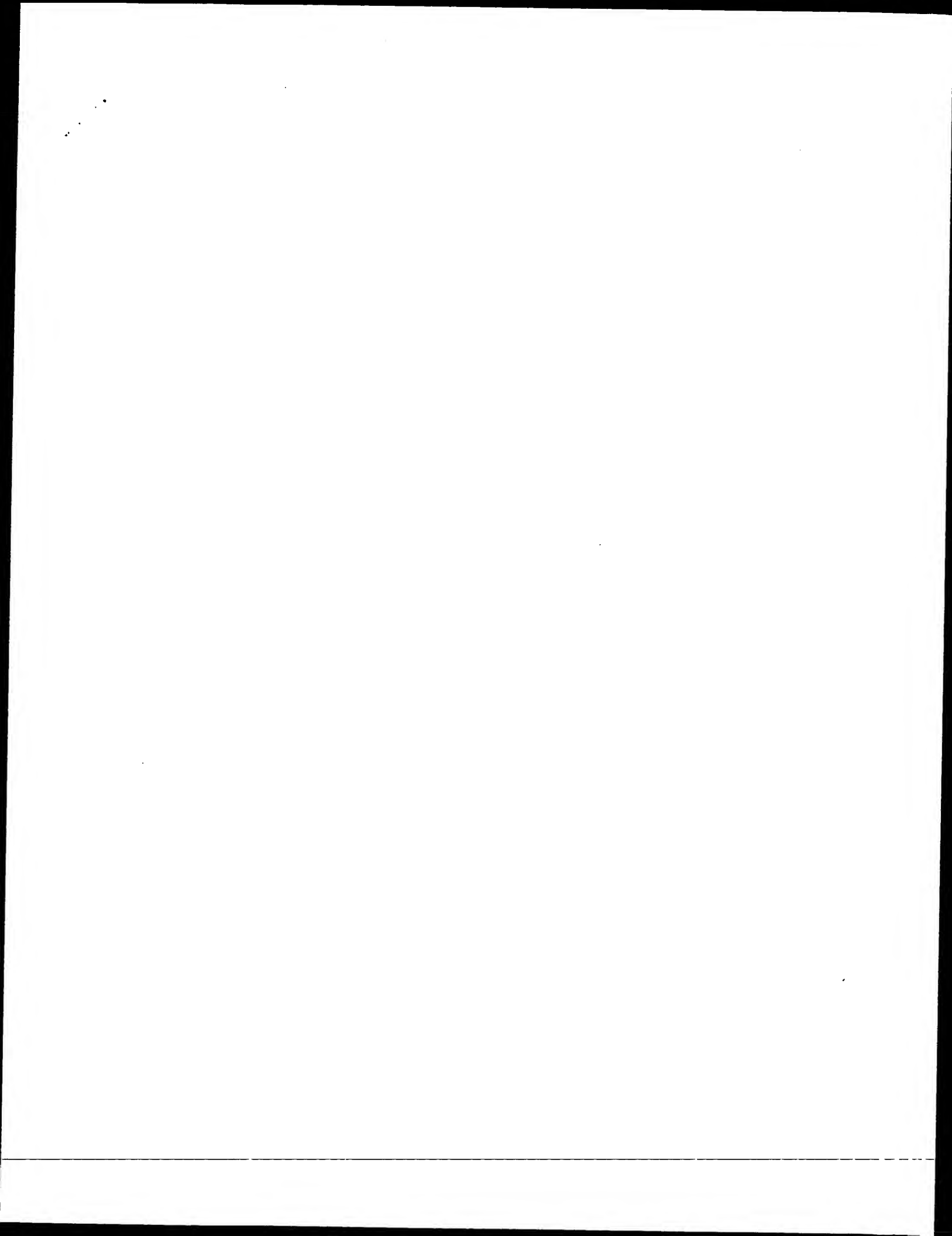
                    Copyright (c) 1993 - 2000 Compugen Ltd.
                                                    GenCore version 4.5

Run on:             May  7, 2002, 12:32:34 ; Search time 21.92 Seconds
                                              (without alignments)
                                              205.738 Million cell updates/sec

Title:
Perfect score:      655
Sequence:           US-09-155-739-11
Sequence:           1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:   100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Database :          SwissProt_39:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length DB	ID	Description
1	427.5	65.3	147	1	P01744	HV1C_HUMAN	homo sapien
2	409	62.4	120	1	P01747	HV03_MOUSE	mus musculu
3	408.5	62.4	139	1	P01751	HV07_MOUSE	mus musculu
4	405	61.8	117	1	P01743	HV1B_HUMAN	homo sapien
5	399	60.9	140	1	P01746	HV02_MOUSE	mus musculu
6	396	60.5	117	1	P23083	HV1G_HUMAN	homo sapien
7	390	59.5	117	1	P01742	HV1A_HUMAN	homo sapien
8	378	57.7	117	1	P01757	HV13_MOUSE	mus musculu
9	375.5	57.3	118	1	P06330	HV51_MOUSE	mus musculu
10	373	56.9	117	1	P01757	HV12_MOUSE	mus musculu
11	371.5	56.7	137	1	P01755	HV11_MOUSE	mus musculu
12	369	56.3	138	1	P03980	HV48_MOUSE	mus musculu
13	364.5	55.6	120	1	P06329	HV50_MOUSE	mus musculu
14	360	55.0	121	1	P01745	HV01_MOUSE	mus musculu
15	360	55.0	136	1	P01759	HV15_MOUSE	mus musculu
16	355	54.2	125	1	P06326	HV1F_HUMAN	homo sapien
17	349.5	53.4	120	1	P80421	HV1H_HUMAN	homo sapien
18	349	53.3	117	1	P01753	HV09_MOUSE	mus musculu
19	344.5	52.6	114	1	P01741	HV00_MOUSE	mus musculu
20	338	51.6	117	1	P01748	HV04_MOUSE	mus musculu
21	336	51.3	117	1	P01750	HV06_MOUSE	mus musculu
22	333.5	50.9	136	1	P01783	HV16_MOUSE	mus musculu
23	333	50.8	117	1	P01754	HV10_MOUSE	mus musculu
24	330.5	50.5	124	1	P01761	HV1E_HUMAN	homo sapien
25	329	50.2	117	1	P01758	HV14_MOUSE	mus musculu
26	329	50.2	117	1	P06328	HV49_MOUSE	mus musculu
27	326	49.8	117	1	P06327	HV42_MOUSE	mus musculu
28	326	49.8	123	1	P01793	HV24_MOUSE	mus musculu
29	325.5	49.7	119	1	P01807	HV37_MOUSE	mus musculu
30	325.5	49.7	124	1	P01760	HV1D_HUMAN	homo sapien
31	324.5	49.5	119	1	P01809	HV38_MOUSE	mus musculu
32	323.5	49.4	119	1	P01810	HV40_MOUSE	mus musculu
33	320.5	48.9	122	1	P01768	HV3G_HUMAN	homo sapien
34	319	48.7	117	1	P01812	HV42_MOUSE	mus musculu
35	318.5	48.6	122	1	P01762	HV3A_HUMAN	homo sapien
36	318	48.5	121	1	P01771	HV3J_HUMAN	homo sapien
37	318	48.5	123	1	P01788	HV19_MOUSE	mus musculu
38	315	48.1	123	1	P01787	HV18_MOUSE	mus musculu
39	314.5	48.0	122	1	P01790	HV21_MOUSE	mus musculu
40	314	47.9	117	1	P01749	HV05_MOUSE	mus musculu
41	313	47.8	123	1	P01794	HV25_MOUSE	mus musculu
42	313	47.8	142	1	P01749	HV39_MOUSE	mus musculu
43	312	47.6	118	1	P01805	HV01_RAT	rattus norv
44	312	47.6	123	1	P01791	HV22_MOUSE	mus musculu
45	311.5	47.6	122	1	P01769	HV3H_HUMAN	homo sapien

ALIGNMENTS

RESULT 1
HV1C_HUMAN

```
ID   HV1C_HUMAN     STANDARD;      PRT;    147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (in) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
RN   [2]
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
DR   PIR; A02026; E1HUND.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    147       IG HEAVY CHAIN V-I REGION ND.
FT   MOD_RES      20     20       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     41    115
FT   CONFLICT     21     21       T -> V (IN REF. 2).
FT   CONFLICT     53     54       IH -> HI (IN REF. 2).
FT   CONFLICT     67     68       VG -> GV (IN REF. 2).
FT   NON_TER     125    125       MISSING (IN REF. 2).
SQ   SEQUENCE   147 AA;  16491 MW;  948F9F72A53666C20 CRC64;
     SEQUENCE OF 20-147.
```

Query Match   65.3%; Score 427.5; DB 1; Length 147;
Best Local Similarity   64.1%; Pred. No. 6.6e-36;
  Matches   82; Conservative 16; Mismatches 25; Indels 5; Gaps 1;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
           ::::::::::::::::::::::::::::::::: : : ::::::: : : :::: :  : :
Db      20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY  79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-----EGYYGNYGVYAMDYWGQ  115
           :: ::::: ::  :::  :::: ::: :::::::::: :     : ::  ::::::::::
Db         ...
```

```
Db    80 APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDIYNFDYSYTLDVWGQ 139

Qy   116 GTLVTVSS 123
         ||  ||||
Db   140 GRTVTVSS 147
```

RESULT 2
```
ID    HV03_MOUSE    STANDARD;    PRT;    120 AA.
AC    P01747;
DT    21-JUL-1986 (Rel. 01, Created)
DT    21-JUL-1986 (Rel. 01, Last sequence update)
DT    15-JUL-1999 (Rel. 38, Last annotation update)
DE    IG HEAVY CHAIN V REGION 36-65.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=83131846; PubMed=6186498;
RA    Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA    Marshak-Rothstein A.;
RT    "The genetic basis of antibody production: the dominant anti-arsonate
RT    idiotype response of the strain A mouse.";
RL    Eur. J. Immunol. 12:1023-1032(1982).
CC    -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC        DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC        CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC        SEGMENT, JH2.
DR    PIR; A02028; HVMSG7.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_V.
DR    Pfam; PF00047; ig; 1.
DR    SMART; SM00406; IGv; 1.
KW    Immunoglobulin V region;
FT    NON_TER    120    120
SQ    SEQUENCE 120 AA; 13307 MW; FF04EA167B654AF CRC64;
```

```
Query Match         62.4%;    Score 409;      DB 1;    Length 120;
Best Local Similarity  63.1%;    Pred. No. 3.7e-34;
Matches    77;    Conservative    18;    Mismatches    25;    Indels    2;    Gaps    1;

Qy     2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD  61
         |||:||||   |||: |||||||| ||||||    ||:||: |||    | | |||||
Db     1 VQLQQSGAELVRAGSSVKMSCKASGYFTTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN  60

Qy    62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVTV 121
         :|:||:||      ||||||:|| :||||:|||||||:        |:|| |||||||:
Db    61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVFYCARSVYYG--GSYFDWGQGTTLTV  118

Qy   122 VSS 123
         |||
Db   119 VSS 120
```

RESULT 3
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ID    HV07_MOUSE    STANDARD;    PRT;    139 AA.
AC    P01751; P01752;
DT    21-JUL-1986 (Rel. 01, Created)
DT    21-JUL-1986 (Rel. 01, Last sequence update)
DT    15-JUL-1999 (Rel. 38, Last annotation update)
DE    IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=C57BL/6;
RX    MEDLINE=81234548; PubMed=6788376;
RA    Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA    Baltimore D.;
RT    "Heavy chain variable region contribution to the NPb family of
RT    antibodies: somatic mutation evident in a gamma 2a variable region.";
RL    Cell 24:625-637(1981).
CC    -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC        MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC        (NPB ANTIBODIES).
```
```
DR    EMBL; J00529; AAA38170.1; -.
DR    PIR; A02034; MHMS18.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_V.
DR    SMART; SM00406; IGv; 1.
DR    Pfam; PF00047; ig; 1.
KW    Immunoglobulin V region; Signal.
FT    SIGNAL       1     19
FT    CHAIN       20    139    IG HEAVY CHAIN V REGION B1-8/186-2.
FT    DOMAIN      20     49    FRAMEWORK 1.
FT    DOMAIN      50     54    COMPLEMENTARITY-DETERMINING 1.
FT    DOMAIN      55     68    FRAMEWORK 2.
FT    DOMAIN      69     85    COMPLEMENTARITY-DETERMINING 2.
FT    DOMAIN      86    117    FRAMEWORK 3.
FT    DOMAIN     118    124    D SEGMENT.
FT    DOMAIN     125    139    JH2 SEGMENT.
FT    DISULFID    41    115    BY SIMILARITY.
FT    NON_TER    139    139
SQ    SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
```

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Query Match         62.4%;    Score 408.5;    DB 1;    Length 139;
Best Local Similarity  62.6%;    Pred. No. 4.9e-34;
Matches    77;    Conservative    18;    Mismatches    25;    Indels    3;    Gaps    1;

Qy     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
         |||||| |||: ||||||| |||||||:| ||  |:|||:|||: ||||| |||| ||||
Db    20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY  79

Qy    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         : |:|:|| || |  ||||||:||||||||:|||||||          |:|| |||||||:
Db    80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYGS---SYFDYWGQGTTLT  136

Qy   121 VSS 123
         |||
Db   137 VSS 139
```

RESULT 4
```
ID    HV1B_HUMAN    STANDARD;    PRT;    117 AA.
AC    P01743;
DT    21-JUL-1986 (Rel. 01, Created)
DT    21-JUL-1986 (Rel. 01, Last sequence update)
DT    15-JUL-1999 (Rel. 38, Last annotation update)
DE    IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=83144028; PubMed=6298778;
RA    Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT    "Evolutionary aspects of immunoglobulin heavy chain variable region
```

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RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-855(1983).
```
```
DR   EMBL; J00240; AAA52988.1; -.
DR   PIR; A02024; HVHUHG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; signal.
FT   SIGNAL     1     19
FT   CHAIN     20    117
FT   NON_TER   117   117
SQ   SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match    61.8%;  Score 405;  DB 1;  Length 117;
Best Local Similarity  79.6%;  Pred. No. 9e-34;
Matches   78;  Conservative  5;  Mismatches  15;  Indels  0;  Gaps  0;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
Db   20  QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY  79

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR  98
Db   80  AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR  117
```

```
RESULT 5
ID   HV02_MOUSE    STANDARD;    PRT;    140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
```
```
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
```

```
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL     1     19
FT   CHAIN     20    140
FT   NON_TER   140   140
SQ   SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CB8 CRC64;

Query Match    60.9%;  Score 399;  DB 1;  Length 140;
Best Local Similarity  61.0%;  Pred. No. 4.4e-33;
Matches   75;  Conservative  19;  Mismatches  27;  Indels  2;  Gaps  1;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
Db   20  EVQLQQSGAELVRAGSSVRMSCKASGYFTSYGINWVKQRPGQGLEWIGYINPNGNGYINY  79

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYYAMDYWGQGTLVT  120
Db   80  NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVFFCARSHYG--GSYDFDVWGQGTPLT  137
```

```
RESULT 6
ID   HVIG_HUMAN    STANDARD;    PRT;    117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
```
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DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVHU35.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; signal.
FT   SIGNAL     1     19
FT   CHAIN     20    117
FT   NON_TER   117   117
SQ   SEQUENCE 117 AA; 13009 MW; BE61CB63F8CE97BD CRC64;

Query Match    60.8%;  Score 396;  DB 1;  Length 117;
Best Local Similarity  78.6%;  Pred. No. 7.1e-33;
Matches   77;  Conservative  5;  Mismatches  16;  Indels  0;  Gaps  0;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
Db   20  QVQLVQSGAEVKKPGASVKVSCKASGYFTGYIMHWVRQAPGQGLEWMGRINPNSGGTNY  79
```

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
         ||||||| || |||||||||||||| |||||| |||||
Db   80 AQKFQGRVTRTDTSISTAYMELSRLRSDDTVVYYCAR 117

RESULT 7
HV1A_HUMAN

ID   HV1A_HUMAN   STANDARD;   PRT;   117 AA.
AC   P01742;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [2]
RP   SEQUENCE.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. XI. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA G-1 C REGION OF THIS
CC   MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR   PIR; A02023; GIHUEU.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID   22   96
FT   NON_TER   1   1
FT   NON_TER   117 117
SQ   SEQUENCE   117 AA;   12472 MW;   99D60ADAEBD52818 CRC64;

DISULFIDE BOND.

PYRROLIDONE CARBOXYLIC ACID.

RESULT 8
HV13_MOUSE

ID   HV13_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION J558.
OS   Mus musculus (Mouse).

Query Match
Best Local Similarity   59.5%;   Score 390;   DB 1;   Length 117;
Matches   84;   Conservative   8;   Mismatches   25;   Indels   6;   Gaps   2;
Pred. No. 2.8e-32;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY 60
         |||||||||||||||| :|| ||||||||: |||| |||||||||||||||| ||| ||
Db   1 QVQLVQSGAEVKKPGSSVSVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
         | ||:|:||| |:|: |:|||||||||||||||| ||: :|||:| |:| |||||| |||
Db   61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-----GGYGIYSPEEY-NGGLVT 114

Qy 121 VSS 123
         |||
Db 115 VSS 117

RESULT 9
HV51_MOUSE

ID   HV51_MOUSE   STANDARD;   PRT;   118 AA.
AC   P06330;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION AC38 205.12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02040; MHMS38.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN   1   98   V SEGMENT.
FT   DOMAIN   99 104   D SEGMENT.
FT   DOMAIN   105 118   J SEGMENT.
FT   DISULFID   22   96   BY SIMILARITY.
FT   NON_TER   118 118
SQ   SEQUENCE   118 AA;   12934 MW;   94F7BEE4C762A018 CRC64;

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC   BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC   WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A26242; MHMSJ5.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER   117 117
FT   DISULFID   22   96
SQ   SEQUENCE   117 AA;   13024 MW;   292E2AF4BE447E41 CRC64;

Query Match
Best Local Similarity   57.7%;   Score 378;   DB 1;   Length 117;
Matches   72;   Conservative   20;   Mismatches   25;   Indels   6;   Gaps   1;
Pred. No. 4.4e-31;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY 60
         :||| :||| ::| |||||:||||||| | ||: | ::|:||: :||||||| | :|
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNGGTSY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT 120
         : ||:|: |: :| : |:|||:: |::| |:|||||||: | ||| |||| |||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-----WYFDVWGAGTTVT 114

Qy 121 VSS 123
         |||
Db 115 VSS 117

us-09-155-739-11.rsp

RESULT 10
HV12_MOUSE

Query Match   57.3%;   Score 375.5; DB 1; Length 118;
Best Local Similarity 58.5%; Pred. No. 8e-31;
Matches 72; Conservative 17; Mismatches 29; Indels 5; Gaps 1;

```
Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         :|:|:|| :|||| ||||||||||| :|:|||||:|:|||||:|:|||:|:|||||
Db   1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         || |:|:| |:|:||| ||| ||||||:|||| |||||||
Db  61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR-----GYGDPFDVWGTGTTVT 115

Qy 121 VSS 123
         |||
Db 116 VSS 118
```

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ID   HV12_MOUSE    STANDARD;    PRT;   117 AA.
AC   P01756;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MOPC 104E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83075344; PubMed=6816276;
RA   Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA   Hood L.E.;
RT   "Complete amino acid sequence of a mouse mu chain: homology among
RT   heavy chain constant region domains.";
RL   Biochemistry 21:5415-5424(1982).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC       PROTEIN HAS ALSO BEEN DETERMINED.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A02039; MHMS4E.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   DISULFID     22     96       BY SIMILARITY.
FT   CARBOHYD     55     55       N-LINKED (GLCNAC...).
FT   NON_TER     117    117
SQ   SEQUENCE  117 AA;  12983 MW;  3CF8ACE4BE447E41 CRC64;
```

RESULT 11
HV11_MOUSE

Query Match   56.9%;   Score 373; DB 1; Length 117;
Best Local Similarity 59.3%; Pred. No. 1.4e-30;
Matches 73; Conservative 19; Mismatches 25; Indels 6; Gaps 2;

```
Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         :|:|:|| :|||| ||||||||||| :|:|||||:|:|||||:|:|||:|:|||||
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         || |:|:| |:|:||| ||| ||||||:|||| |:|:|
Db  61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD-----YDWY-FDVWGAGTTVT 114

Qy 121 VSS 123
         |||
Db 115 VSS 117
```

```
ID   HV11_MOUSE    STANDARD;    PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN      20     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   DOMAIN     118    122       D SEGMENT.
FT   DOMAIN     123    137       JH2 SEGMENT.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    137    137
SQ   SEQUENCE  137 AA;  15200 MW;  ADD5881BF44B88EC9 CRC64;
```

RESULT 12
HV48_MOUSE

Query Match   56.7%;   Score 371.5; DB 1; Length 137;
Best Local Similarity 60.2%; Pred. No. 2.4e-30;
Matches 74; Conservative 14; Mismatches 30; Indels 5; Gaps 2;

```
Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||| ||| |:| |||||| ||||||| :|:||||||:|||||:|:|||:|:||||||
Db  20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         |||| ||| |:|:|||||:|:|||| ||:|:|| ||||| |:|:||:|:||||||
Db  80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-RLGRY-----FDVWGQGTLVT 134

Qy 121 VSS 123
         |||
Db 135 VSS 137
```

```
ID   HV48_MOUSE    STANDARD;    PRT;   138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
```

```
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; signal.
FT   SIGNAL        1     20
FT   CHAIN        21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN       21     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    127       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      128    138       FRAMEWORK 4.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;

Query Match             56.3%;  Score 369;  DB 1;  Length 138;
Best Local Similarity   58.1%;
Matches    72;  Conservative   20;  Mismatches   26;  Indels   6;  Gaps   2;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
            ||| | ||| :|| |||||:|:|||||||  ::|||||:|||:| | | |: | | | |
Db   20  QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY   79

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLV  119
            |: |: :|:| |:|||||||||||| ||||||| : ||||||||  ||||||||
Db   80  NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYYDWF----VYWGQGTLV  134
```

```
RESULT 13
ID   HV50_MOUSE     STANDARD;    PRT;  120 AA.
AC   P06329;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION AC38 15.3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02037; MHMS15.
DR   InterPro; IPR003006; Ig_MHC.
```

```
RESULT 14
ID   HV01_MOUSE     STANDARD;    PRT;  121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
DR   PIR; A02027; GVMS11.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     98
FT   DOMAIN       99    105       V SEGMENT.
FT   DOMAIN      106    120       D SEGMENT.
FT   DOMAIN      106    120       J SEGMENT.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13311 MW;  914453F426F09834 CRC64;

Query Match             55.6%;  Score 364.5;  DB 1;  Length 120;
Best Local Similarity   56.1%;
Matches    69;  Conservative   19;  Mismatches   32;  Indels   3;  Gaps   1;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
            ||| |  | :|:||||||:|:|||||:|| |:|:||::| |||:| || : ||:| | |
Db    1  QVQLLQPGTELVKPGASVNLSCKASGYTFTSYWMHWIRQRPGQGLEWIGGINPSNGGTNY   60

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
            :||: :|:| ||:|||: ||||:| | ||:|||||||| |:|    :||  ||:||:|||
Db   61  NEKFRSKATLTVDKSSSATYMQLSTPTSEDSAVYYCARWDYEGD---RYFDVWGTGTTVT  117
```

```
Query Match             55.0%;  Score 360;  DB 1;  Length 121;
Best Local Similarity   55.3%;
Matches    68;  Conservative   23;  Mismatches   30;  Indels   2;  Gaps   2;

Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60
            ||| | ||| :|| |||||:|:|||:| |:|:|:|||||::| |||:| || | |:| |
Db    1  EAQLQQSGAELVRPGTSVKISCKAAGYIFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY   60

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
Db   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120
```

```
Db        61  NDNLKGKATLTADTSSSTAVIQLSSLTSEDSAIYHCAR-GIIYNSSPY-FDSWGQGTTLT 118
              :: .: ||||||::|||:.|||| |||:.|||| |||:| | ||||| ::|

Qy       121  VSS 123
              |||
Db       119  VSS 121
```

```
RESULT  15
HV15_MOUSE
ID      HV15_MOUSE          STANDARD;        PRT;     136 AA.
AC      P01759;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=82222262; PubMed=6806821;
RA      Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA      Blattner F.R.;
RT      "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT      by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT      by two adjacent CH genes.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC      -----------------------------------------------------------------------
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----------------------------------------------------------------------
DR      EMBL; J00494; AAA38130.1; -.
DR      PIR; A02042; HVMSB1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL          1     19
FT      CHAIN          20    136       IG HEAVY CHAIN V REGION BCL1.
FT      NON_TER        136   136
SQ      SEQUENCE    136 AA;    15078 MW;    6827CFBC6DB3F35E CRC64;
```

```
Query Match             55.0%;    Score 360;  DB 1;  Length 136;
Best Local Similarity   56.9%;    Pred. No. 3.3e-29;
Matches   70;  Conservative  17;  Mismatches  30;  Indels  6;  Gaps  2;

Qy       1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
            |||| ||| |||| || ||||| ||| ||||: |:||||::||:|.|.:|||| | ||
Db      20  QVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79

Qy      61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
            : |||:: |:|:| :||| :|||:|: |:| ||||||  ||||| |||||||| :|
Db      80  NQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR---YYGNY---FDYWGQGTTLT 133

Qy     121  VSS 123
            |||
Db     134  VSS 136
```

Search completed: May 7, 2002, 12:32:34
Job time: 565 sec

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OM protein - protein search, using sw model

GenCore version 4.5

Run on: May 7, 2002, 12:31:42 ; Search time 67.26 Seconds
                       (without alignments)
                       267.492 Million cell updates/sec

Title: us-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL.17:*
                1: sp_archea:*
                2: sp_bacteria:*
                3: sp_fungi:*
                4: sp_human:*
                5: sp_invertebrate:*
                6: sp_mammal:*
                7: sp_mhc:*
                8: sp_organelle:*
                9: sp_phage:*
                10: sp_plant:*
                11: sp_rodent:*
                12: sp_virus:*
                13: sp_vertebrate:*
                14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%Query Match	Match length	DB	ID	Description
1	457.5	69.8	124	4	Q9UL92	Q9UL92 homo sapien
2	440	67.2	468	11	Q9JL31	Q9JL31 mus musculu
3	432	66.0	109	11	Q9JL85	Q9JL85 mus musculu
4	432	66.0	119	4	Q9UL94	Q9UL94 homo sapien
5	428	65.3	119	5	Q9GZ2	Q9GZ2 schistosoma
6	428	65.3	125	4	Q9UL95	Q9UL95 homo sapien
7	422	64.4	473	11	Q9DBL4	Q9DBL4 mus musculu
8	411.5	62.8	116	4	Q9UL89	Q9UL89 homo sapien
9	408.5	62.4	473	11	Q99L25	Q99L25 mus musculu
10	407	62.1	117	11	Q90XE9	Q90XE9 mus musculu
11	399	60.9	150	4	Q9Y298	Q9Y298 homo sapien
12	398.5	60.8	500	4	Q9BRV0	Q9BRV0 homo sapien
13	386.5	58.9	118	11	Q9ZIC4	Q9ZIC4 mus musculu
14	386	58.9	117	11	Q9QXF0	Q9QXF0 mus musculu
15	384	58.6	157	4	Q95978	Q95978 homo sapien
16	381.5	58.2	463	11	Q99IC4	Q99IC4 mus musculu
17	380	58.0	484	11	Q99LA6	Q99LA6 mus musculu
18	379.5	57.9	109	11	Q9JL75	Q9JL75 mus musculu
19	374.5	57.2	110	11	Q9JL77	Q9JL77 mus musculu

20	371.5	56.7	114	11	Q9JL81	Q9JL81 mus musculu
21	342.5	52.3	110	11	Q9JL83	Q9JL83 mus musculu
22	338	51.6	111	11	Q9D9B8	Q9D9B8 mus musculu
23	334	51.0	111	11	Q9Z1C6	Q9Z1C6 mus musculu
24	333	50.8	120	4	Q9BUA1	Q9BUA1 homo sapien
25	326.5	49.8	487	11	Q99KA4	Q99KA4 mus musculu
26	325.5	49.7	298	11	Q90YF0	Q90YF0 mus musculu
27	322.5	49.2	147	4	Q9Y509	Q9Y509 homo sapien
28	322	49.2	113	4	Q9U190	Q9U190 homo sapien
29	320.5	48.9	118	4	Q9UL72	Q9UL72 homo sapien
30	319.5	48.8	112	4	Q9HCC1	Q9HCC1 homo sapien
31	314	47.9	116	4	Q9UL93	Q9UL93 homo sapien
32	311	47.5	131	4	Q9UL88	Q9UL88 homo sapien
33	304	46.4	121	4	Q9UL71	Q9UL71 homo sapien
34	300.5	45.9	121	11	Q99NG4	Q99NG4 mus musculu
35	297.5	45.4	122	4	Q9UL84	Q9UL84 homo sapien
36	290	44.3	119	4	Q9UL73	Q9UL73 homo sapien
37	288.5	44.0	124	6	Q9N0W4	Q9N0W4 oryctolagus
38	286.5	43.7	118	4	Q9UL91	Q9UL91 homo sapien
39	286	43.7	597	4	Q9BQB8	Q9BQB8 homo sapien
40	285.5	43.6	124	6	Q9N0W6	Q9N0W6 oryctolagus
41	285	43.5	597	4	Q9BU10	Q9BU10 homo sapien
42	279	42.6	104	4	Q9UL87	Q9UL87 homo sapien
43	275	42.0	479	11	Q99M22	Q99M22 mus musculu
44	273.5	41.8	437	11	Q9R1A4	Q9R1A4 mus musculu
45	271	41.4	102	11	Q9JL79	Q9JL79 mus musculu

ALIGNMENTS

RESULT   1
Q9UL92

ID   Q9UL92;   PRELIMINARY;   PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035022; AAD56258.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1.
FT   NON_TER   124   124.
SQ   SEQUENCE   124 AA;   13580 MW;   1BAAACBD96ACD2A2 CRC64;

Query Match   69.8%;   Score 457.5;   DB 4;   Length 124;
Best Local Similarity   69.8%;   Pred. No. 5.1e-40;
Matches   91;   Conservative   9;   Mismatches   16;   Indels   15;   Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          :|||:|:|||||||||||||::|:|||||||| |:|||||||||||||||:|:| | |
Db   1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMIHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM---------DY 112
          |||||| || ||| | || || || |||| ||||||||| |||||||| ||
Db   61 ...

```
Db    61 AQKFQQGRVTMPRDTSTSTVYMELSSLRSEDTAVYYCAR-------GLYVVVPAAFSRFDY 113
            |||||||||||
Qy   113 WGQGTLVTVSS 123
            |||||||||||
Db   114 WGQGTLVTVSS 124


RESULT 2
ID   Q99L31                    PRELIMINARY;      PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TREMBLrel. 17, Created)
DT   01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
SQ   SEQUENCE   468 AA;  51661 MW;  96352328B3332ADB CRC64;

Query Match             67.2%;  Score 440;  DB 11;  Length 468;
Best Local Similarity   67.5%;  Pred. No. 1.7e-37;
Matches    83; Conservative  16; Mismatches  20; Indels   4; Gaps   1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||| ||| ||:||:|:|| || ||||||||||||  ||:||:||  |:||:|| :|
Db   20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGYNGVYAMDYWGQGTLVT 120
          |||| ||:| :|| ||:||  ||||||||||||||||  |||  |:||||||||||| |
Db   80 APKFQDKAPITADTSSNTAYLQLSSLTSEDTAIYYCARNLIYGGY---YDYWGQGTTIT 135

Qy  121 VSS 123
          |||
Db  136 VSS 138


RESULT 3
ID   Q9JL85                    PRELIMINARY;      PRT;   109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TREMBLrel. 15, Created)
DT   01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206021; AAF69319.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER    1     1
FT   NON_TER  109   109
SQ   SEQUENCE   109 AA;  11944 MW;  DFE615FB6CED4EDE CRC64;
```

```
Query Match             66.0%;  Score 432;  DB 11;  Length 109;
Best Local Similarity   68.7%;  Pred. No. 1.9e-37;
Matches    79; Conservative  15; Mismatches  15; Indels   6; Gaps   1;

Qy    9 AEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKFQGRV 68
          |:  ||||||| || ||||||||||:||:|:||||  ||:|||  |:|||||||||:|||
Db    1 AELVKPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60

Qy   69 TITADTSASTAYMELSSLRSEDTAVYYCAREGYGYNGVYAMDYWGQGTLVTVSS 123
          ||||:|| ||:||  ||||||||||||||  |||  |:||||||||||| |||
Db   61 TITSDTSSNTAYLQLSSLTSEDTAIYYCVRR-------GAVVFDYWGQGTALTVSS 109


RESULT 4
ID   Q9JL94                    PRELIMINARY;      PRT;   119 AA.
AC   Q9JL94;
DT   01-MAY-2000 (TREMBLrel. 13, Created)
DT   01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035020; AAD56256.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER    1     1
FT   NON_TER  119   119
SQ   SEQUENCE   119 AA;  13205 MW;  13E64F5345F4A16E CRC64;

Query Match             66.0%;  Score 432;  DB 4;  Length 119;
Best Local Similarity   70.7%;  Pred. No. 2.1e-37;
Matches    87; Conservative  10; Mismatches  22; Indels   4; Gaps   1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||| |||||||||||||||||||||:||:|:||||  ||:|||  |:|||||||
Db    1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPNSWTTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGYNGVYAMDYWGQGTLVT 120
          ||||||:|||| :|| ||:||  ||||||||||||||  |||  |:||||||||||||
Db   61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW-----FDPWGQGTLVT 116

Qy  121 VSS 123
          |||
Db  117 VSS 119


RESULT 5
ID   Q9GYZ2                    PRELIMINARY;      PRT;   119 AA.
AC   Q9GYZ2;
DT   01-MAR-2001 (TREMBLrel. 16, Created)
DT   01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
```

```
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC   Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC   Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the heavy chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF282622; AAG01452.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13567 MW;  BA893873FD5FA6AB CRC64;

Query Match             65.3%;  Score 428;  DB 5;  Length 119;
Best Local Similarity   66.7%;  Pred. No. 5,5e-37;
Matches   82;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||| |||||:|||||| |||||||:|:| | |:|||||| || |:|  : ||||  |
Db    1 QVQLVESGAEVRKPGASVSVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYY--AMDYWGQGTLVT 120
         :|:||||| |||  | ||||| |:|||||:|||||||    || |||||   | ||||||||
Db   61 NQKFKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCAR--YYDDH--YCLDYWGQGTTVT 116

Qy  121 VSS 123
         |||
Db  117 VSS 119


RESULT   6
Q9UL95
ID   Q9UL95     PRELIMINARY;      PRT;   125 AA.
AC   Q9UL95;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035019; AAD56255.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
```

```
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  13516 MW;  0D3CD5C232488EAC CRC64;

Query Match             65.3%;  Score 428;  DB 4;  Length 125;
Best Local Similarity   68.8%;  Pred. No. 5,9e-37;
Matches   86;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||| |||||||||||||||||||||:|:| | |:||||||| ||||| :|:  ||| |
Db    1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYY--AMDYWGQGTL 118
         :|:||||| ||  || ||||||| |||||:||||||||   |||  | |   | :||||||
Db   61 AQKVQGRVTMTTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120

Qy  119 VTVSS 123
         |||||
Db  121 VTVSS 125


RESULT   7
Q9D8L4
ID   Q9D8L4     PRELIMINARY;      PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1810006009RIK PROTEIN.
GN   1810006009RIK
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AK007918; BAB25349.1; -.
DR   MGD; MGI:1924014; 1810006009Rik.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
```

SQ   SEQUENCE   473 AA; 51699 MW; 9DED57A51A475FBB CRC64;

Query Match
Best Local Similarity   64.4%;   Score 422; DB 11;   Length 473;
Matches   81; Conservative   19; Pred. No. 1.3e-35; Mismatches   19; Indels   4; Gaps   2;

```
Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY   60
            |||| :|||| |:|||||:|||||| : |  :  |.||:| || |||:|
Db   20  QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYV  79

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT  120
            :|:|:| |:||| ||||||:|||| |||:|||:||:||   |   |  ||||||||||||
Db   80  NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY--DYDWFA--YWGQGTLVT  135

Qy  121  VSS  123
            ||:
Db  136  VSA  138
```

RESULT 8
ID   Q9UL89   PRELIMINARY;   PRT;   116 AA.
AC   Q9UL89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035025; AAD56261.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
NON_TER   1   1
NON_TER   116   116
SEQUENCE   116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match
Best Local Similarity   62.8%;   Score 411.5; DB 4;   Length 116;
Matches   87; Conservative   3; Pred. No. 2.8e-35; Mismatches   25; Indels   5; Gaps   2;

```
Qy    5  VOSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKYDPKF   64
            |||||||||| ||||||||||| | .:  | |:||||| |||||||| |. | || |
Db    1  VOSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKF  60

Qy   65  QGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY-AMDYWGQGTLVTVSS  123
            |||||||| | ||||||||||||||||||||||||          :||| ||:|||||||
Db   61  QGRVTITADKSTSTAYMELSSLRSEDTAVYYCAS----SNNGPYWYFDLWGRGTLVTVSS  116
```

RESULT 9
ID   Q99L25   PRELIMINARY;   PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
SEQUENCE   473 AA; 52449 MW; BE9889B79B6DA155 CRC64;

Query Match
Best Local Similarity   62.4%;   Score 408.5; DB 11;   Length 473;
Matches   79; Conservative   18; Pred. No. 3.2e-34; Mismatches   25; Indels   25; Gaps   2;

```
Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY   60
            |||| :| |||:||||||:|||.|| : |  :  | ||:|| :| |||||
Db   20  QVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRPEQGGLEWIGYIVPRDGSTYV  79

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYYAMDYWGQGTL  118
            :|:|:| |:||| ||||||:|.|| |||:|| :|:|.      | | | ||||||||
Db   80  NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGSSIYG-YGLYYFDYDYWGQGTT  138

Qy  119  VTVSS  123
            :||||
Db  139  ITVSS  143
```

RESULT 10
ID   Q90XE9   PRELIMINARY;   PRT;   117 AA.
AC   Q90XE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AJ225174; CAB65237.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
NON_TER   1   1
NON_TER   117   117
SEQUENCE   117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match
Best Local Similarity   62.1%;   Score 407; DB 11; Length 117;
Matches   77; Conservative   19; Pred. No. 8.1e-35; Mismatches   21; Indels   6; Gaps   1;

```
Qy    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWRQAPGQRLEWMGRIDPANGYTKY   60
            :|| | | |:||||||||:||||||| | .  | | | |  |||||  |:| |.|.
Db    1  EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWVKQSHGKSLEWIGDINPNNGGTSY   60

Qy   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYYAMDYWGQGTLVT  120
            :|:|:| |:||.| |||||||:|.|| |||:||||||:|      | ||||||||::|
Db   61  NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-----YAMDYWGQGTSVT  114

Qy  121  VSS  123
            |||
Db  115  VSS  117
```

RESULT 11

```
Q9Y298
ID   Q9Y298      PRELIMINARY;      PRT;   150 AA.
AC   Q9Y298;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN   IGG VH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98322155; PubMed=9657749;
RA   Jacquemin M.G., Vander Elst L.P.L.;
RT   "Mechanism and kinetics of factor VIII inactivation: study with an
RT   IgG4 monoclonal antibody derived from a hemophilia A patient with
RT   inhibitor.";
RL   Blood 92:496-506(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ224083; CAA11829.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Signal.
FT   SIGNAL        1     19
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16031 MW;  563D164AB22802D5 CRC64;      POTENTIAL.
```

```
Query Match             60.9%;  Score 399;  DB 4;  Length 150;
Best Local Similarity   65.0%;  Pred. No. 7.5e-34;
Matches   80;  Conservative   12;  Mismatches   25;  Indels    6;  Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||||||||||| |||:||||||||||||||||||||||| || : |
Db   20 QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
        :||| ||||||||| |||||||||||||:||||||| ||  |||||
Db   80 AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP------DPDAFDIWGQGTMVT 133

Qy  121 VSS 123
        |||
Db  134 VSS 136
```

RESULT 12

```
Q9BRV0
ID   Q9BRV0      PRELIMINARY;      PRT;   500 AA.
AC   Q9BRV0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE   UNKNOWN (PROTEIN FOR MGC:14588).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PROSTATE;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005951; AAH05951.1; -.
SQ   SEQUENCE   500 AA;  54154 MW;  0A9BF43F2A3CC6D9 CRC64;
```

```
Query Match             60.8%;  Score 398.5;  DB 4;  Length 500;
Best Local Similarity   63.3%;  Pred. No. 3.7e-33;
Matches   81;  Conservative   10;  Mismatches   32;  Indels    5;  Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||:||||||||  |||||:||||:||||  ||  : |||||||||||||||||| :: ||
Db   20 QVHLVQSGAEVMSPGASVRVSCKTSGYAFHYYSIIWVRQAPGQGLEWMGWISPSSDNTRF 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-----EGYYGNYGVYAMDYWGQ 115
        ||||:||||| ||||| || ||||||||||||||| |||     ||  :: || ||||
Db   80 AKKFQGRVTLITDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCQNDYYYYMDVWGK 139

Qy  116 GTLVTVSS 123
        || |||||
Db  140 GTIVTVSS 147
```

RESULT 13

```
Q921C4
ID   Q921C4      PRELIMINARY;      PRT;   118 AA.
AC   Q921C4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA   Matis L.M., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; U78801; AAD00293.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13036 MW;  90EEC559D31EC4FC CRC64;
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```
Query Match             59.0%;  Score 386.5;  DB 11;  Length 118;
Best Local Similarity   59.5%;  Pred. No. 1.1e-32;
Matches   75;  Conservative   18;  Mismatches   22;  Indels   11;  Gaps    2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        |||:||||||   ||||||:||||||| |:| |  ||| : |||| ||||| :  : ||
Db    1 QVQVQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNGVYAMDYWGQGT 117
        :||:|||.|| || ||||||| |||||||||||||||||    ||:||
Db   61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYF------DYWGGGT 112

Qy  118 LVTVSS 123
        |||||
Db  113 TLTVSS 118
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RESULT 14

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Q9QXF0
ID   Q9QXF0      PRELIMINARY;      PRT;   117 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 13, Last sequence update)
```

```
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1     1
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA;   13060 MW;   D81GAD0858A47E4C CRC64;
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Query Match   58.9%;   Score 386;   DB 11;   Length 117;
Best Local Similarity   59.7%;   Pred. No. 1.2e-32;
Matches   74;   Conservative   20;   Mismatches   22;   Indels   8;   Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        |||||||||:|.:||.||||:|:|||||||||||:|||||||||||||||||||||||||
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE-GYYGNYGVYAMDYWGQGTLV 119
        :|||.:|:|.:||:.|||||||||||:|||||||||||| ||:||||||||||||:
Db  61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDY-------FDYWGQGTTL 113

Qy 120 TVSS 123
        ||||
Db 114 TVSS 117
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RESULT 15
ID   O95978
AC   O95978;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VH1 PROTEIN PRECURSOR (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RA   Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA   Bohlen H., Diehl V., Wolf J.;
RT   "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT   patient with mixed cellularity Hodgkin's disease is associated with
RT   somatic mutations within the untranslated regions of rearranged and
RT   class switch recombined Ig genes.";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ005570; CAA06599.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Signal.
FT   SIGNAL    1     21
FT   NON_TER   157   157
SQ   SEQUENCE   157 AA;   17304 MW;   86986EDDA84088B5 CRC64;
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Query Match   58.6%;   Score 384;   DB 4;   Length 157;
Best Local Similarity   63.2%;   Pred. No. 2.8e-32;
Matches   79;   Conservative   10;   Mismatches   30;   Indels   6;   Gaps   2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||:||.||||:|:|||||||||||:||||||||||...|||.|||||||||.
Db  20 QVQLVQSGAEIKRPGASVKVHCKTSGYVFTSYYIHWVRQPRGQGLEWMGGIGPCVGGSTMC 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYY--GNYGVYAMDYWGQGTL 118
        :||||:|::||.|||||||||||||:||||||||||.:|| |||||||||||||||
Db  80 AEKFQGRLTMTRNTSTTVYMELSRLRFEDTAVYFCGRGGRWRSGNYN----GHWGQGTP 135

Qy 119 VTVSS 123
        |||||
Db 136 VTVSS 140
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Search completed: May 7, 2002, 12:31:42
Job time: 628 sec

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          GenCore version 4.5
          Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:              May 7, 2002, 12:18:19 ; Search time 67.39 Seconds
                                              (without alignments)
                                              138.496 Million cell updates/sec

Title:               US-09-155-739-2
Perfect score:       680
Sequence:            1 MRPSIQFLGLLLFWLHGAQC..........YCLQYDNLWTFGGGTKLEIK 126
Scoring table:       BLOSUM62
                     Gapop 10.0 , Gapext 0.5
Searched:            522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters:    522463

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   A_Geneseq_1101:*
             1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
             2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
             3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
             4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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            11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
            12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
            13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result          Query                    %
No.    Score    Match  Length  DB ID        Description
----   -----    -----  ------  -----        -----------
 1     680      100.0   126    16   AAR81326  Mouse VLA-4 antibo
 2     680      100.0   126    16   AAR81332  Human VLA-4 reshap
 3     680      100.0   126    18   AAW22409  Alpha-4 integrin m
 4     634       93.2   128    15   AAR60627  ME1-14 light chain
 5     619       91.0   126    18   AAW22419  Humanised alpha-4
 6     618.5     91.0   126    11   AAR06252  Variable region of
 7     569       83.7   106    16   AAR81328  Mouse anti-VLA-4 a
 8     539       79.3   359    20   AAY22913  Human MCP-3 and mu
 9     539       79.3   359    20   AAY22911  Human MCP-3 and mu
10     535       78.7   374    20   AAY29916  Artificial synthet
11     510.5     75.1   107    16   AAR78970  Light chain variab
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ALIGNMENTS

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RESULT          1
AAR81326

ID   AAR81326 standard; Protein; 126 AA.
XX
AC   AAR81326;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key              Location/Qualifiers
FH
FT   Peptide          1..20
FT                    /note= "signal peptide"
FT   Region           21..43
FT                    /note= "framework region 1"
FT   Region           44..54
FT                    /note= "complementarity determining region 1"
FT   Region           55..69
FT                    /note= "framework region 2"
FT   Region           70..76
FT                    /note= "complementarity determining region 2"
FT   Region           77..108
FT                    /note= "framework region 3"
FT   Region           109..116
FT                    /note= "complementarity determining region 3"
FT   Region           117..126
FT                    /note= "framework region 4"
XX
PN   WO9519790-A1.
```

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12    508   74.7   106   16   AAR81321   Humanized anti-VLA
13    508   74.7   106   16   AAW22412   Humanised alpha-4
14    508   74.7   108   17   AAR93159   Murine monoclonal
15    508   74.7   637   13   AAR26983   (FRP51)-ETA fusion
16    507   74.6   245   19   AAW26800   Anti-gp54 MAb T16
17    503   74.0   109   19   AAW26797   Anti-gp54 MAb T16
18    503   74.0   240   19   AAR85495   ScFv(FWP51). Synt
19    501   73.7   355   18   AAW35133   R. pipiens recombi
20    500   73.5   109   12   AAR13658   Murine OKT4A light
21    500   73.5   241   13   AAR26981   FWP51 fusion prote
22    479.5  70.5   234   22   AAR13050   CD4-specific CDR-g
23    468    68.3   234   18   AAB81995   Ganglioside GD3 sp
24    462.5  68.0   128   22   AAW10233   Ganglioside GD3 sp
25    457.5  67.3   129   15   AAR57482   Humanized 1308F VL
26    456.5  67.1   129   17   AAR92085   Humanised antibody
27    456.5  67.1   129   15   AAR47207   Human/murine IL-1
28    455.5  67.0   128   18   AAB81997   Ganglioside GD3 sp
29    452.5  66.5   128   22   AAR12359   Light (kappa) chai
30    452.5  66.5   127   12   AAY56724   Amino acid sequenc
31    451.5  66.4   129   21   AAY56721   Ganglioside GD3 sp
32    448.5  66.0   128   22   AAB81993   Anti-human CD23 sp
33    447.5  65.8   129   19   AAW70379   Mouse MAb 1C11 L c
34    446.5  65.7   126   12   AAR12237   Anti-human CD23 5E
35    446.5  65.7   129   14   AAR30880   PXOM2. Mus muscul
36    445.5  65.5   132   18   AAW22842   Human anti-tumour
37    443.5  65.2   130   21   AAY56737   Human anti-tumour
38    442    65.0   124   21   AAY56719   Amino acid sequenc
39    441    64.9   237   21   AAY96301   Human IGFAM-13 imm
40    438.5  64.5   128   17   AAW01527   Monoclonal antibod
41    438.5  64.5   128   21   AAY24990   Monoclonal antibod
42    438.5  64.5   127   14   AAR39265   Mouse C4G1 Ig ligh
43    437.5  64.3   127   19   AAW49809   Variable region of
44    437.5  64.3   131   16   AAR84553   MAb SCH94.03 light
45    436.5  64.2   128   22   AAB81999   Ganglioside GD3 sp
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Left column

```
XX
PD   27-JUL-1995.
XX
PF
XX
PR   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99889.
XX
PS   Disclosure; Fig 1; 105pp; English.
XX
CC
CC   The sequence represents the mouse antibody 21.6 light chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.
CC   cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;
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Query Match Best Local Similarity 100.0%; Score 680; DB 16; Length 126;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 mrpsiqflglllfwlhgaqcdiqmtqspsslsaslggkvvitcktsqdinkymawyqhkp 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 gkrprlllhytsalqpgipsrfsgsgsgsgrdysfnisnlepediatyyclqydnlwtfggg 120

Qy  121 TKLEIK 126
          ||||||
Db  121 tkleik 126
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RESULT   2
AAR81332
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ID   AAR81332 standard; Protein; 126 AA.
AC   AAR81332;
XX
DT   23-MAR-1996 (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
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Right column

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XX
FH   Key                 Location/Qualifiers
XX
FT   Peptide             1..20
FT                       /note= "signal peptide"
FT   Region              21..43
FT                       /note= "framework region 1"
FT   Region              44..54
FT                       /note= "complementarity determining region 1"
FT   Region              55..69
FT                       /note= "framework region 2"
FT   Region              70..76
FT                       /note= "complementarity determining region 2"
FT   Region              77..108
FT                       /note= "framework region 3"
FT   Region              109..116
FT                       /note= "complementarity determining region 3"
FT   Region              117..126
FT                       /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF
XX
PR   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99893.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 10; 105pp; English.
XX
CC
CC   The sequence represents the human reshaped antibody 21.6 light
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
CC   then subcloned into mammalian cell expression vectors containing
CC   human kappa or gamma-1 constant regions. In the humanized light
CC   chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells. The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis. They can also be used in the treatment of
CC   stroke, cerebral traumas, meningitis or encephalitis. The
CC   antibodies can also be used for detecting VLA-4, for affinity
CC   purification or for generating anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;
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Query Match Best Local Similarity 100.0%; Score 680; DB 16; Length 126;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVVITCKTSQDINKYMAWYQHKP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 mrpsiqflglllfwlhgaqcdiqmtqspsslsaslggkvvitcktsqdinkymawyqhkp 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 gkrprlllhytsalqpgipsrfsgsgsgsgrdysfnisnlepediatyyclqydnlwtfggg 120
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Qy   121 TKLEIK 126
             |||||
Db   121 tkleik 126

RESULT  3
ID   AAW22409 standard; Protein; 126 AA.
XX
AC   AAW22409;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VL region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
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FT                   /label= Leader
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /label= FR4
FT                   /note= "framework region 4"
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PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74759.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 68; 107pp; English.
XX
CC   This polypeptide comprises the light chain variable region (VL) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC   complementarity determining regions (CDRs) of the 21.6 VL can be
CC   incorporated into a human REI framework to produce a claimed
CC   humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, tumour, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence  126 AA;

Query Match      100.0%;  Score 680;  DB 18;  Length 126;
Best Local Similarity  100.0%;  Pred. No. 1.2e-47;
Matches  126;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  mrpsiqflglillfwlhgaqcdiqmtqspsslsaslggkvtitcktsqdinkymawyqhkp   60

Qy   61  GKRPRLLIHYTSALQPGIPSRFSGSGSGGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  gkrprllihytsalqpgipsrfsgsgsggrdysfnisnlepediatyyclqydnlwtfggg  120

Qy   121 TKLEIK 126
             |||||
Db   121 tkleik 126

RESULT  4
ID   AAR60627 standard; Protein; 128 AA.
XX
AC   AAR60627;
XX
DT   04-JUN-1995  (first entry)
XX
DE   ME1-14 light chain variable region.
XX
KW   Monoclonal antibody; tumour.
XX
OS   Homo sapiens.
XX
PN   WO9421294-A.
XX
PD   29-SEP-1994.
XX
PF   14-MAR-1994;   94WO-US02724.
XX
PR   19-MAR-1993;   93US-0033864.
XX
PA   (BIGN/) BIGNER D D.
PA   (CARR/) CARREL S.
PA   (ZALU/) ZALUTSKY M R.
XX
PI   Bigner DD, Carrel S, Zalutsky MR;
XX
DR   WPI; 1994-316669/39.
DR   N-PSDB; AAQ73537.
XX
PT   Method of treating solid or cystic tumours with antibodies - by
PT   administering monoclonal antibody ME1-14, having Fc deleted,
PT   using injection or deposition in the cyst cavity
XX
PS   Disclosure; Fig 2; 31pp; English.
XX
CC   The sequence is that of the ME1-14 light chain. The protein is a
CC   monoclonal antibody which can be administered to treat solid or
```

```
CC   cystic tumours.
CC   See also AAR60626.
XX
SQ   Sequence   128 AA;

Qy   Query Match   93.2%;   Score 634;   DB 15;   Length 128;
     Best Local Similarity   93.8%;   Pred. No. 5.9e-44;
     Matches 118;   Conservative  3;   Mismatches  5;   Indels   0;   Gaps   0;

Qy         1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 mrpsiqflglllfwlhgahcdiqmtqspsslsaslggkvtitckasqdinkyiawyqhkp 60

Qy        61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 gkgprllmhytslqpgipsrfsgsgsgrdysfsisnlepediatyyclqydnlltfggg 120

Qy       121 TKLEIK 126
             ||||||
Db       121 tkleik 126

RESULT   5
ID   AAW22419 standard; Protein; 126 AA.
XX
AC   AAW22419;
XX
DT   08-DEC-1997   (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key               Location/Qualifiers
FT
FT   Peptide           1..20
FT                     /label= Leader
FT   Protein           21..126
FT                     /label= Mat_protein
FT                     /note= "VL version La (Claim 25)"
FT   Region            21..43
FT                     /label= FR1
FT                     /note= "REI framework region 1"
FT   Region            44..54
FT                     /label= CDR1
FT                     /note= "21.6 complementarity determining region 1"
FT   Region            55..69
FT                     /label= FR2
FT                     /note= "REI framework region 2"
FT   Region            70..76
FT                     /label= CDR2
FT                     /note= "21.6 complementarity determining region 2"
FT   Region            77..108
FT                     /label= FR3
FT                     /note= "REI framework region 3"
FT   Region            109..116
FT                     /label= CDR3
FT                     /note= "21.6 complementarity determining region 3"
FT   Region            117..126
FT                     /label= FR4
FT                     /note= "REI framework region 4"
XX
PN   WO9718838-A1.
```

```
XX
PD   29-MAY-1997.
XX
PD   21-NOV-1996;
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
PF   WPI; 1997-297879/27.
DR   N-PSDB; AAI74788.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 10; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22412). It is composed of complementarity determining regions from
CC   the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human REI framework. It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;

Qy   Query Match   91.0%;   Score 619;   DB 18;   Length 126;
     Best Local Similarity   90.5%;   Pred. No. 9.2e-43;
     Matches 114;   Conservative  6;   Mismatches  6;   Indels   0;   Gaps   0;

Qy         1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
             ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||| |
Db         1 mrpsiqflglllfwlhgaqcdiqmtqspsslsasvgdrvtitcktsqdinkymawyqqtp 60

Qy        61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
             ||||||||||||||||||||||||||||||:|||:|||||||||||||||||||||||| |
Db        61 gkaprllhytsalqpgipsrfsgsgsgrdyttisslqpediatyyclgydnlwtfggg 120

Qy       121 TKLEIK 126
             ||:|||
Db       121 tkveik 126

RESULT   6
ID   AAR06252 standard; protein; 128 AA.
XX
AC   AAR06252;
XX
DT   10-DEC-1990   (first entry)
XX
DE   Variable region of murine AHT 107 light chain.
XX
KW   Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
OS   Mus sp.
XX
PN   EP380068-A.
XX
PD   01-AUG-1990.
```

```
XX
PF   24-JAN-1990;  90EP-0101351.
XX
PR   04-DEC-1989;  89US-0441702.
PR   24-JAN-1989;  89US-0301216.
XX
PA   (MOLE-) MOLECULAR THERAPEU.
XX
PI   Zerler B;
XX
DR   WPI: 1990-232892/31.
DR   N-PSDB; AAQ05556.
XX
PS   Disclosure; ; P; English.
XX
PT   Expression vectors for producing chimeric monoclonal antibodies -
PT   which express human constant region and non-human variable region
XX
CC   MAbs comprising mouse CH and CL constant regions whith human
CC   variable regions may be used to create mouse/human hybrid MAbs,
CC   which have a longer serum half-life. Method can be used to produce
CC   Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ   Sequence  128 AA;

Query Match             91.0%;  Score 618.5;  DB 11;  Length 128;
Best Local Similarity   88.2%;  Pred. No. 1e-42;
Matches 112;  Conservative  12;  Mismatches   2;  Indels   1;  Gaps   1;

Qy          1 MRPSIQFGLLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
              ||||||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||
Db          1 mrpsiqfglllfwlhgaqcdiqmtqspsslsaslggkvtitcktsqdinkfiawyqhkp 60

Qy         61 GKRPRLLIHYTSALQPGIPSRFSGSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
              |:||||||||||:|| ||||||||||||:||||||:|||||||||||||:||| |||||
Db         61 gegprlilhytslqppipsrfsgsgsgskdysfsinnlepediatyyclryddlpwtfgg 120

Qy        120 GTKLEIK 126
              ||||| ::
Db        121 gtklevr 127

RESULT   7
AAR81328
ID   AAR81328 standard; Protein; 106 AA.
XX
AC   AAR81328;
XX
DT   02-APR-1996  (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX

FH   Key             Location/Qualifiers
FH
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "mouse light chain variable framework
FT                   region 1"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "mouse light chain variable complementarity
FT                   determining region 1"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "mouse light chain variable framework
FT                   region 2"
FT   Region          50..56
FT                   /label= CDR2
```

```
FT                   /note= "mouse light chain variable complementarity
FT                   determining region 2"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "mouse light chain variable framework
FT                   region 3"
FT   Region          89..96
FT                   /label= CDR3
FT                   /note= "mouse light chain variable complementarity
FT                   determining region 3"
FT   Region          97..106
FT                   /label= FR4
FT                   /note= "mouse light chain variable framework
FT                   region 4"
XX
XX
PN   WO9517790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI: 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 66; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ98895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence  106 AA;

Query Match             83.7%;  Score 569;  DB 16;  Length 106;
Best Local Similarity  100.0%;  Pred. No. 8e-39;
Matches 106;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 60

Qy         81 RFSGSGSGGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
              ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtklelk 106

RESULT   8
AAY29913
ID   AAY29913 standard; Protein; 359 AA.
```

XX
AC   AAY29913;
XX
DT   17-NOV-1999 (first entry)
XX
DE   Human MCP-3 and murine scFv38 fusion protein.
XX
KW   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW   immune response; HIV; infection.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
XX
PN   WO9946392-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999; 99WO-US05345.
XX
PR   12-MAR-1998; 98US-0077745.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kwak LW, Biragyn A;
XX
DR   WPI; 1999-551418/46.
XX
PT   New fusion polypeptides comprising a chemokine and a tumour antigen or
PT   HIV antigen, used for treating cancers or treating or preventing HIV
PT   infection -
XX
PS   Disclosure; Page 118-119; 142pp; English.
XX
CC   The present invention describes fusion proteins comprising a chemokine
CC   and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC   comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC   Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC   (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC   SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC   HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC   gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC   be used for producing an immune response, e.g. an effector T cell immune
CC   response. They can also be used for treating cancer or treating or
CC   preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC   can be used in in vitro diagnostic assays, as well as in screening assays
CC   for identifying unknown tumour antigen epitopes and fine mapping of
CC   tumour antigen epitopes. The present sequence represents a fusion protein
CC   from the present invention.
XX
SQ   Sequence   359 AA;

Query Match   79.3%; Score 539; DB 20; Length 359;
Best Local Similarity   91.8%; Pred. No. 6.7e-36;
Matches 101; Conservative   4; Mismatches   5; Indels   0; Gaps   0;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          |:||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   229 gsgsdiqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqp 288

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||||||||||||||||||||||||||||:|||||||||||||||||
Db   289 gipsrfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 338

XX
DE   Human IP-10 and murine scFv38 fusion protein.
XX
KW   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW   immune response; HIV; infection.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
XX
PN   WO9946392-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999; 99WO-US05345.
XX
PR   12-MAR-1998; 98US-0077745.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kwak LW, Biragyn A;
XX
DR   WPI; 1999-551418/46.
XX
PT   New fusion polypeptides comprising a chemokine and a tumour antigen or
PT   HIV antigen, used for treating cancers or treating or preventing HIV
PT   infection -
XX
PS   Disclosure; Page 115-116; 142pp; English.
XX
CC   The present invention describes fusion proteins comprising a chemokine
CC   and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC   comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC   Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC   (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC   SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC   HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC   gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC   be used for producing an immune response, e.g. an effector T cell immune
CC   response. They can also be used for treating cancer or treating or
CC   preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC   can be used in in vitro diagnostic assays, as well as in screening assays
CC   for identifying unknown tumour antigen epitopes and fine mapping of
CC   tumour antigen epitopes. The present sequence represents a fusion protein
CC   from the present invention.
XX
SQ   Sequence   361 AA;

Query Match   79.3%; Score 539; DB 20; Length 361;
Best Local Similarity   91.8%; Pred. No. 6.7e-36;
Matches 101; Conservative   4; Mismatches   5; Indels   0; Gaps   0;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          |:||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   231 gsgsdiqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqp 290

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||||||||||||||||||||||||||||:|||||||||||||||||
Db   291 gipsrfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 340

RESULT 10
AAY29916
ID   AAY29916 standard; Protein; 374 AA.
XX
AC   AAY29916;
XX
DT   17-NOV-1999 (first entry)
XX
DE   Artificial synthetic construct protein SEQ ID NO:15.
XX
KW   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;

RESULT   9
AAY29911
ID   AAY29911 standard; Protein; 361 AA.
XX
AC   AAY29911;
XX
DT   17-NOV-1999 (first entry)

KW   immune response; HIV; infection.
OS   Synthetic.
XX
PN   WO9946392-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US05345.
XX
PR   12-MAR-1998;   98US-0077745.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kwak LW, Biragyn A;
XX
DR   WPI; 1999-551418/46.
XX
PS   Disclosure: Page 117-118; 142pp; English.

The present invention describes fusion proteins comprising a chemokine
and a tumour antigen or HIV antigen. Specifically claimed fusion
proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
human SDF-1 and human IP-10 and HIV gp120; (6) human
MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
can be used for producing an immune response, e.g. an effector T cell
immune response. They can also be used for treating cancer or treating
or preventing HIV infection. The fusion proteins and/or nucleotide
sequences can be used in in vitro diagnostic assays, as well as in
screening assays for identifying unknown tumour antigen epitopes and fine
mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
sequences given in the present invention but which
are not mentioned further within the specification.

SQ   Sequence   374 AA;

Query Match   78.7%;   Score 535;   DB 20;   Length 374;
Best Local Similarity   94.3%;   Pred. No. 1.5e-35;
Matches 100;   Conservative   3;   Mismatches   3;   Indels   0;   Gaps   0;

```
Qy    21 DIQMTQSPSSLSASLGGKVYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    95 digmtqspsslsaslggkvtitckasqdinkylawyghkpgkgprllihytstlqppgips 154

Qy    81 RFSGSGSGRDYSFENISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
         ||||||||||||||||||||||||||||||| : |||||||||||||
Db   155 rfsgsgsgrdysfsisnlepediatyycylqydnlytfgggtkleik 200
```

XX
PD   03-AUG-1995.
XX
PF   27-JAN-1995;   95WO-US01199.
XX
PR   27-JAN-1994;   94US-0187407.
XX
PA   (BION-) BIONEBRASKA INC.
XX
PI   Lopez O, Wagner FW, Wylie DE;
XX
DR   WPI; 1995-2754415/36.
DR   N-PSDB; AAQ97508.
XX
PS   Claim 23; Page 67-68; 106pp; English.

Hybridoma antibodies have been produced with the spleen cells of
BALB/c mouse that had received multiple injections of mercuric ions
reacted with glutathione to produce a mercuric ion coordinate
covalent compound which was covalently bound to keyhole limpet
hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
5B6 and 3E8) were producing MAbs that were strongly positive
against glutathione-mercuric ions but negative against glutathione
without mercuric ions. RNA was isolated from hybridoma cells with
guanidine isothiocyanate. First strand cDNA synthesis was catalysed
by MuLv reverse transcriptase. The primers used for cDNA synthesis
were complementary to the 5' end of the CH1 domain of the heavy
chain expressed by the hybridoma of interest, or to the 5' and of
the C kappa domain. Some of the primers used for cDNA synthesis are
shown in AAQ97510-Q97518. The primer used for cDNA synthesis of the
variable region of a particular antibody polypeptide was also used
for PCR amplification of that variable region, in conjunction with
an appropriate V-region primer. In addition, the VH primer AAQ97518
was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
of the PCR amplified nucleotides were determined. These are given
in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
and in the claims are different from the descriptions in the
sequence listings. The descriptions in the sequence listings are
used here.

SQ   Sequence   107 AA;

Query Match   75.1%;   Score 510.5;   DB 16;   Length 107;
Best Local Similarity   91.6%;   Pred. No. 4e-34;
Matches 98;   Conservative   3;   Mismatches   5;   Indels   1;   Gaps   1;

```
Qy    21 DIQMTQSPSSLSASLGGKVYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     1 digmtqspsslsaslggkvtitckasqdinkylawyghkpgkgprllihytstlqppgips 60

Qy    81 RFSGSGSGRDYSFENISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
         |||||||||||||||||||||||||||||||||| ||||||||||||
Db    61 rfsgsgsgrdysfsisnpepediatyycylqydnslftgsgtkleik 107
```

XX
PT   New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT   monoclonal antibodies, used for detecting, removing, adding or
PT   neutralising heavy metals

XX

RESULT 11
AC   AAR78970
ID   AAR78970 standard; Protein; 107 AA.
XX
AC   AAR78970;
XX
DT   21-DEC-1995 (first entry)
XX
DE   Light chain variable region for monoclonal antibody 23F8.
XX
KW   Monoclonal antibody; heavy metal; mercury; variable region;
KW   light chain.
XX
OS   Synthetic.
XX
PN   WO9520607-A.

RESULT 12
AC   AAR81321
ID   AAR81321 standard; Protein; 106 AA.
XX
AC   AAR81321;
XX
DT   02-APR-1996 (first entry)
XX
DE   Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.

```
XX
OS   Chimeric Mus musculus.
OS   Chimeric Homo sapiens.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 9; Page 67; 105pp; English.
XX
CC   The sequence encodes the humanized mouse antibody 21.6 light chain
CC   variable region, La, directed against leukocyte adhesion molecule
CC   VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC   AAQ99892) regions are linked to human constant regions in the
CC   construction of a humanized antibody against VLA-4. The 5' and 3'
CC   ends of the mouse cDNAs are modified using PCR primers (see
CC   AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC   containing human kappa or gamma-1 constant regions. In the humanized
CC   light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC   VR framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 L chain. Plasmids encoding the chimeric
CC   antibodies are transfected into COS cells. The humanized antibodies
CC   can be used for inhibiting adhesion of a leukocyte to an endothelial
CC   cell and for treating inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence    106 AA;

Query Match             74.7%;  Score 508;  DB 16;  Length 106;
Best Local Similarity   88.7%;  Pred. No. 6.3e-34;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||||||||| :| ::||||||||||||||| ||| || |||||:||||||||||||
Db     1 diqmtqspslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60

Qy    81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
         |||||||||| :|:||:|||||||||||||| ||||||||| |||:|||
Db    61 rfsgsgsgrdytftissiqpediatyclqydnlwtfgggtkveik 106

RESULT  13
AAW22412
ID   AAW22412 standard; Protein; 106 AA.
XX
AC   AAW22412;
XX
DT   08-DEC-1997   (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL La.
XX
KW   Alpha-4 Integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
```

```
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key            Location/Qualifiers
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FT   Region         1..23
FT                  /label= FR1
FT                  /note= "REI framework region 1"
FT   Region         24..34
FT                  /label= CDR1
FT                  /note= "21.6 complementarity determining region 1"
FT   Region         35..49
FT                  /label= FR2
FT                  /note= "REI framework region 2"
FT   Misc-difference 45
FT                  /note= "REI Lys-45 is substd. by Lys of mouse
FT                  21.6 VL, important in supporting the
FT                  CDR2 loop"
FT   Misc-difference 49
FT                  /note= "REI Tyr-49 is substd. by His of mouse
FT                  21.6 VL, located at the binding site"
FT   Region         50..56
FT                  /label= CDR2
FT                  /note= "21.6 complementarity determining region 2"
FT   Region         57..88
FT                  /label= FR3
FT                  /note= "REI framework region 3"
FT   Misc-difference 58
FT                  /note= "REI Val-58 is substd. by Ile of mouse
FT                  21.6 VL, important in supporting the CDR2
FT                  loop"
FT   Misc-difference 69
FT                  /note= "REI Thr-69 is substd. by Arg of mouse
FT                  21.6 VL, involved in antibody-antigen
FT                  binding"
FT   Region         89..96
FT                  /label= CDR3
FT                  /note= "21.6 complementarity determining region 3"
FT   Region         97..106
FT                  /label= FR4
FT                  /note= "REI framework region 4"
FT   Misc-difference 103
FT                  /note= "REI Leu-103 substd. by Val, more typical
FT                  of human kappa light chain J region"
FT   Misc-difference 104
FT                  /note= "REI Gln-104 substd. by Glu, more typical
FT                  of human kappa light chain J region"
FT   Misc-difference 106
FT                  /note= "REI Thr-106 substd. by Lys, more typical
FT                  of human kappa light chain J region"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 25; Fig 6; 107pp; English.
XX
```

```
CC        This polypeptide, designated La, comprises the light chain variable
CC        region (VL) of a humanised alpha-4 integrin antibody 21.6.  It is
CC        composed of complementarity determining regions (CDRs) from the VL
CC        region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC        21.6 and a modified human REI framework. It can be expressed in
CC        mammalian host cells following PCR amplification and mutagenesis
CC        of appropriate fragments of mouse and human DNA sequences. The
CC        humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC        to produce a claimed humanised 21.6 antibody that is useful in the
CC        manufacture of a medicament for treating asthma, atherosclerosis,
CC        AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC        arthritis, transplant rejection, graft versus host disease, tumour
CC        metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC        ischaemia, and acute leukocyte mediated lung injury. The antibody
CC        may also be used in the affinity purification of alpha-4 integrin
CC        for use as a vaccine or an immunogen. It is also useful for
CC        generating idiotypic antibodies. The humanised antibody has a
CC        half-life in the human circulation essentially equivalent to that
CC        of naturally occurring human antibodies.
XX
SQ        Sequence      106 AA;

Query Match             74.7%;  Score 508;  DB 18;  Length 106;
Best Local Similarity   88.7%;  Pred. No. 6.3e-34;
Matches  94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||||||||||||||||||||| || ||||||||||||||||||||||
Db       1 diqmtqspsslsasvgdrvticcktsqdinkymawygqtpgkaprllihytsalqpgips 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||||:||:|||||||||||||||||||| |||:|||
Db      61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgggtkveik 106
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RESULT 14
ID   AAR93159
AAR93159 standard; Protein; 108 AA.
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AC   AAR93159;
XX
DT   24-OCT-1996  (first entry)
XX
DE   Murine monoclonal antibody K20 kappa chain variable region.
XX
KW   Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW   beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW   T cell activation; complementarity determining region; CDR.
OS   Mus musculus.
XX
FH   Key              Location/Qualifiers
FH
FT   Region           1..23
FT                    /label= FR1
FT                    /note= "framework region"
FT   Region           24..34
FT                    /label= CDR1
FT                    /note= "complementarity determining region"
FT   Region           35..49
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FT                    /note= "framework region"
FT   Region           50..56
FT                    /label= CDR2
FT                    /note= "complementarity determining region"
FT   Region           57..88
FT                    /label= FR3
FT                    /note= "framework region"
FT   Region           89..94
FT                    /label= CDR3
FT                    /note= "complementarity determining region"
FT   Region           95..108
FT                    /label= J_kappa1
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XX
PN   FR2724393-A1.
XX
PD   15-MAR-1996.
XX
PF   12-SEP-1994;  94FR-0010858.
XX
PR   12-SEP-1994;  94FR-0010858.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (PROT-) PROTEINE PERFORMANCE SA.
XX
PI   Bernard A,  Cervoni MF,  Lefranc MP,  Margaritte C;
PI   Poul MA;
XX
PS   Example 1; Fig 2A; 39pp; French.
XX
CC        The present sequence is that of the variable region of the kappa
CC        light chain from murine monoclonal antibody K20. The antibody
CC        recognises the beta 1 subunit (CD29) of integrins and inhibits
CC        activation and proliferation of peripheral T cells induced by
CC        anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC        for humanisation; the humanised version may be useful as an
CC        immunosuppressant. In the humanisation process, the complementarity
CC        determining regions (CDRs) of a human antibody with framework
CC        regions 70-95% homologous to those of K20 were replaced by the K20
CC        CDRs.
XX
SQ        Sequence      108 AA;

Query Match             74.7%;  Score 508;  DB 17;  Length 108;
Best Local Similarity   89.6%;  Pred. No. 6.4e-34;
Matches  95; Conservative   5; Mismatches   6; Indels   0; Gaps   0;

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           |||:||||||||||||||||| ||||||||||||||||| ||||||||||||||||||
Db       1 diqltqspsslsasiggkvttcckasqdinkyiawyqhepgkgsprllirytsklesgips 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||:|||||||||||||||||||:| |||||:|||||
Db      61 rfsgsgsgrdytfsisnlepediatyyclqyynlwtfgggtkleik 106
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RESULT 15
ID   AAR26983
AAR26983 standard; Protein; 637 AA.
XX
AC   AAR26983;
XX
DT   11-FEB-1993  (first entry)
XX
DE   (FRP51)-ETA fusion protein.
XX
KW   Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2;
KW   variable region; ETA.
OS   Pseudomonas aeruginosa.
XX
FH   Key              Location/Qualifiers
FH
FT   Peptide          1..21
FT                    /label= ompA_signal_peptide
FT   Peptide          22..29
FT                    /label= FLAG_peptide_and_enterokinase_cleavage_site
FT   Domain           33..152
FT                    /label= FWP51_heavy_chain_variable_domain
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FT   Peptide          153..167
FT                    /label= Linker
FT   Domain           168..274
FT                    /label= FRP5_light_chain_variable_domain
FT   Protein          276..397
FT                    /label= ETA_252-613
XX
PN   EP502812-A.
XX
PD   09-SEP-1992.
XX
PF   27-JAN-1992;   92EP-0810056.
-XX
PR   05-FEB-1991;   91EP-0810079.
XX
PA   (CIBA ) CIBA GEIGY AG.
XX
PI   Groner B,   Hardman N,  Harwerth I,  Hynes NE,  Wels WS;
PI   Zwickl M;
XX
DR   WPI; 1992-302096/37.
DR   N-PSDB; AAQ28263.
XX
PS   Disclosure; Page 53-58; 67pp; English.
XX
CC   The sequences given in AAR26982-3 contain part of the exotoxin A (ETA)
CC   sequence corresponding to positions 252-613 of the full exotoxin A
CC   sequence.  These sequences are encoded by Fv(FRP5)-ETA fusion genes.
CC   The ETA sequence was used as a marker gene so that E. coli transformed
CC   with the fusion gene could be identified.  The fusion genes were
CC   expressed in E. coli and the antibodies were extracted.  These
CC   recombinant antibodies can be used for the qualitative and
CC   quantitative determination of c-erbB-2.  This can be used for
CC   monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
XX
SQ   Sequence   637 AA;
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Recombinant antibodies directed to growth factor receptor C-erbB-2 -
for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
or ovarian tumours

```
Query Match   74.7%;   Score 508;  DB 13;  Length 637;
Best Local Similarity   86.4%;   Pred. No. 3.6e-33;
Matches   95;  Conservative   5;  Mismatches   10;  Indels   0;  Gaps   0;

Qy     17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
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Qy     77 GIPSRFSGSGSGRDYSFNISNLPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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Db    224 gipsrfsgsgsgrdysfsihnlepediatyyclhydylyifgggtkleik 273
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Job time: 245 sec
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OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: May 7, 2002, 12:20:09 ; Search time 32.41 Seconds
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Post-processing:

Title: US-09-155-739-2
Perfect score: 680
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Scoring table: BLOSUM62
  Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680	100.0	126	2	US-08-561-521-2	Sequence 2, Appli
2	680	100.0	126	2	US-08-561-521-15	Sequence 15, Appli
3	680	100.0	126	5	PCT-US95-01219-2	Sequence 2, Appli
4	680	100.0	126	5	PCT-US95-01219-15	Sequence 15, Appli
5	634	93.2	128	1	US-08-339-582-4	Sequence 4, Appli
6	569	83.7	106	1	US-08-561-521-5	Sequence 5, Appli
7	569	83.7	106	2	PCT-US95-01219-5	Sequence 5, Appli
8	510.5	75.1	107	2	US-08-888-366-22	Sequence 22, Appli
9	508	74.7	106	2	US-08-561-521-7	Sequence 7, Appli
10	508	74.7	106	5	PCT-US95-01219-7	Sequence 7, Appli
11	508	74.7	637	2	US-08-235-838-16	Sequence 16, Appli
12	508	74.7	637	2	US-08-465-473B-16	Sequence 16, Appli
13	503	74.0	241	2	US-08-235-838-11	Sequence 11, Appli
14	503	74.0	241	2	US-08-465-473B-11	Sequence 11, Appli
15	501	73.7	355	3	US-08-875-811-57	Sequence 57, Appli
16	438.5	64.5	128	2	US-08-259-372A-14	Sequence 14, Appli
17	438.5	64.5	128	1	US-08-468-671-14	Sequence 14, Appli
18	437.5	64.3	127	4	US-08-516-5	Sequence 5, Appli
19	437.5	64.3	127	4	US-08-348-548-4	Sequence 4, Appli
20	437.5	64.3	127	1	PCT-US95-15716-4	Sequence 4, Appli
21	437.5	64.3	131	1	US-08-236-520-2	Sequence 2, Appli
22	437.5	64.3	131	5	PCT-US95-05262-2	Sequence 2, Appli
23	430.5	63.3	138	2	US-08-480-434-63	Sequence 63, Appli
24	430.5	63.3	138	2	US-08-480-434-63	Sequence 63, Appli
25	429.5	63.2	127	3	US-08-836-561-71	Sequence 71, Appli
26	428.5	63.0	129	1	US-08-217-918-2	Sequence 2, Appli
27	426.5	62.7	127	1	US-08-137-117D-37	Sequence 37, Appli
28	426.5	62.7	127	2	US-08-436-717-37	Sequence 37, Appl
29	424.5	62.4	127	3	US-08-649-100-17	Sequence 17, Appl
30	423.5	62.3	236	1	US-08-157-101A-5	Sequence 5, Appl
31	418.5	61.5	142	2	US-08-579-940-2	Sequence 2, Appl
32	418.5	61.5	142	4	US-08-838-692-4	Sequence 4, Appl
33	417.5	61.4	127	1	US-08-137-117D-29	Sequence 29, Appl
34	417.5	61.4	127	2	US-08-436-717-29	Sequence 29, Appl
35	417.5	61.4	127	3	US-08-933-983-7	Sequence 7, Appl
36	416.5	61.2	127	2	US-08-621-751A-6	Sequence 6, Appl
37	416.5	61.2	127	2	US-08-836-561-88	Sequence 88, Appl
38	414.5	61.0	128	2	US-08-470-139-26	Sequence 26, Appl
39	413.5	60.8	125	2	US-08-039-198B-12	Sequence 12, Appl
40	413.5	60.8	125	2	US-08-182-067-2	Sequence 2, Appl
41	413.5	60.8	125	2	US-08-465-313-2	Sequence 2, Appl
42	413.5	60.8	127	1	US-08-649-100-33	Sequence 33, Appl
43	412.5	60.7	127	5	US-09-136-315-8	Sequence 8, Appl
44	410.5	60.4	127	3	US-08-933-983-17	Sequence 17, Appl
45	410.5	60.4	128	4	US-08-569-147-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-2
Sequence 2, Application US/08561521
Patent No. 5840299

GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-2

Query Match 100.0%; Score 680; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.3e-59;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 TKLEIK 126

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Query Match       100.0%;   Score 680;  DB 2;   Length 126;
Best Local Similarity    100.0%;   Pred. No. 1.3e-59;
Matches 126;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

US-08-561-521-15
   MOLECULE TYPE: protein
      TOPOLOGY: linear
      TYPE: amino acid
      LENGTH: 126 amino acids
   SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 15:
      TELEFAX: 415-543-5043
      TELEPHONE: 415-543-9600
   TELECOMMUNICATION INFORMATION:
      REFERENCE/DOCKET NUMBER: 15270-14
      REGISTRATION NUMBER: 30,223
      NAME: Smith, William L.
   ATTORNEY/AGENT INFORMATION:
      FILING DATE: 25-JAN-1994
      APPLICATION NUMBER: US/08/186,269A
   PRIOR APPLICATION DATA:
      CLASSIFICATION: 424
      FILING DATE:
      APPLICATION NUMBER: US/08/561,521
   CURRENT APPLICATION DATA:
      SOFTWARE: PatentIn Release #1.0, Version #1.25
      OPERATING SYSTEM: PC-DOS/MS-DOS
      COMPUTER: IBM PC compatible
      MEDIUM TYPE: Floppy disk
   COMPUTER READABLE FORM:
      ZIP: 94105
      COUNTRY: USA
      STATE: California
      CITY: San Francisco
      STREET: One Market Plaza, Steuart Tower, Suite 2000
      ADDRESSEE: Townsend and Townsend Khourie and Crew
   CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES: 45
   TITLE OF INVENTION: Adhesion Molecule VLA-4
   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
   APPLICANT: Jones, S. Tarran
   APPLICANT: Saldanha, Jose
   APPLICANT: Leger, Olivier J.
   APPLICANT: Bendig, Mary M.
GENERAL INFORMATION:
Patent No. 5840299
Sequence 15, Application US/08561521
US-08-561-15
RESULT 2
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Qy 121 TKLEIK 126
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Db 121 TKLEIK 126

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       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query Match       100.0%;   Score 680;  DB 5;   Length 126;
Best Local Similarity    100.0%;   Pred. No. 1.3e-59;
Matches 126;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

PCT-US95-01219-2
   MOLECULE TYPE: protein
      TOPOLOGY: linear
      TYPE: amino acid
      LENGTH: 126 amino acids
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      TELEFAX: 415-543-5043
      TELEPHONE: 415-543-9600
   TELECOMMUNICATION INFORMATION:
      REFERENCE/DOCKET NUMBER: 15270-14
      REGISTRATION NUMBER: 30,223
      NAME: Smith, William L.
   ATTORNEY/AGENT INFORMATION:
      FILING DATE: 25-JAN-1994
      APPLICATION NUMBER: US 08/186,269
   PRIOR APPLICATION DATA:
      CLASSIFICATION:
      FILING DATE: 25-JAN-1995
      APPLICATION NUMBER: PCT/US95/01219
   CURRENT APPLICATION DATA:
      SOFTWARE: PatentIn Release #1.0, Version #1.25
      OPERATING SYSTEM: PC-DOS/MS-DOS
      COMPUTER: IBM PC compatible
      MEDIUM TYPE: Floppy disk
   COMPUTER READABLE FORM:
      ZIP: 94105
      COUNTRY: USA
      STATE: California
      CITY: San Francisco
      STREET: One Market Plaza, Steuart Tower, Suite 2000
      ADDRESSEE: Townsend and Townsend Khourie and Crew
   CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES: 45
   TITLE OF INVENTION: Adhesion Molecule VLA-4
   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
   APPLICANT: Jones, S. Tarran
   APPLICANT: Saldanha, Jose
   APPLICANT: Leger, Olivier J.
   APPLICANT: Bendig, Mary M.
GENERAL INFORMATION:
Sequence 2, Application PCT/US9501219
PCT-US95-01219-2
RESULT 3
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Qy 121 TKLEIK 126
       ||||||
Db 121 TKLEIK 126

   APPLICANT: Bendig, Mary M.
GENERAL INFORMATION:
Sequence 15, Application PCT/US9501219
PCT-US95-01219-15
RESULT 4
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; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-US95-01219-15

Query Match   100.0%;   Score 680; DB 5;   Length 126;
Best Local Similarity   100.0%;   Pred. No. 1.3e-59;
Matches 126; Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy 121 TKLEIK 126
         ||||||
Db 121 TKLEIK 126

RESULT 5
US-08-339-582-4
; Sequence 4, Application US/08339582
; Patent No. 5558852
; GENERAL INFORMATION:
; APPLICANT: Bigner, Darell D.
; APPLICANT: Zalutsky, Michael R.
; APPLICANT: Carrel, Stefan
; TITLE OF INVENTION: METHOD OF TREATMENT
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: NO. 5558852th Carolina

; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,582
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/033,864
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3175
; TELEFAX: 919-420-2200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-582-4

Query Match   93.2%;   Score 634; DB 1;   Length 128;
Best Local Similarity   93.7%;   Pred. No. 4.2e-55;
Matches 118; Conservative 3;   Mismatches 5;   Indels 0;   Gaps 0;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   1 MRPSIQFLGLLLFWLHGAHCDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
         |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKGPRLLMHYTSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGG 120

Qy 121 TKLEIK 126
         ||||||
Db 121 TKLEIK 126

RESULT 6
US-08-561-521-5
; Sequence 5, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521

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;   FILING DATE:
;   CLASSIFICATION:              424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:          US/08/186,269A
;   FILING DATE:                 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME:                        Smith, William L.
;   REGISTRATION NUMBER:         30,223
;   REFERENCE/DOCKET NUMBER:     15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:                   415-543-9600
;   TELEFAX:                     415-543-5043
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:                      106 amino acids
;   TYPE:                        amino acid
;   STRANDEDNESS:                single
;   TOPOLOGY:                    linear
;   MOLECULE TYPE:               protein
US-08-561-521-5

Query Match             83.7%;  Score 569;  DB 2;  Length 106;
Best Local Similarity   100.0%;  Pred. No. 7.6e-49;
Matches   106;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        ||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
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RESULT   7
PCT-US95-01219-5
Sequence 5, Application PCT/US9501219
;   GENERAL INFORMATION:
;   APPLICANT:                   Bendig, Mary M.
;   APPLICANT:                   Leger, Olivier J.
;   APPLICANT:                   Saldanha, Jose
;   APPLICANT:                   Jones, S. Tarran
;   TITLE OF INVENTION:          Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION:          Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES:         45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:                   Townsend and Townsend Khourie and Crew
;   STREET:                      One Market Plaza, Steuart Tower, Suite 2000
;   CITY:                        San Francisco
;   STATE:                       California
;   COUNTRY:                     USA
;   ZIP:                         94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:                 Floppy disk
;   COMPUTER:                    IBM PC compatible
;   OPERATING SYSTEM:            PC-DOS/MS-DOS
;   SOFTWARE:                    Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:          PCT/US95/01219
;   FILING DATE:                 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:          US 08/186,269
;   FILING DATE:                 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME:                        Smith, William L.
;   REGISTRATION NUMBER:         30,223
;   REFERENCE/DOCKET NUMBER:     15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:                   415-543-9600
;   TELEFAX:                     415-543-5043
;   INFORMATION FOR SEQ ID NO: 5:
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;   SEQUENCE CHARACTERISTICS:
;   LENGTH:                      106 amino acids
;   TYPE:                        amino acid
;   STRANDEDNESS:                single
;   TOPOLOGY:                    linear
;   MOLECULE TYPE:               protein
PCT-US95-01219-5

Query Match             83.7%;  Score 569;  DB 5;  Length 106;
Best Local Similarity   100.0%;  Pred. No. 7.6e-49;
Matches   106;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        ||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
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```
RESULT   8
US-08-888-366-22
Sequence 22, Application US/08888366
;   Patent No. 5972656
;   GENERAL INFORMATION:
;   APPLICANT:                   Lopez, Osvaldo
;   APPLICANT:                   Wylie, Dwane E.
;   APPLICANT:                   Wagner, Fred W.
;   TITLE OF INVENTION:          Mercury Binding Polypeptides and Nucleotides Coding Therefo
;   NUMBER OF SEQUENCES:         39
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:                   Merchant & Gould
;   STREET:                      90 South 7th Street, 3100 No. 5972656west Ctr.
;   CITY:                        Minneapolis
;   STATE:                       MN
;   COUNTRY:                     USA
;   ZIP:                         55402
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:                 Floppy disk
;   COMPUTER:                    IBM PC compatible
;   OPERATING SYSTEM:            PC-DOS/MS-DOS
;   SOFTWARE:                    Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:          US/08/888,366
;   FILING DATE:                 03-JUL-1997
;   CLASSIFICATION:              435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:          US 07/990,542
;   FILING DATE:                 14-DEC-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:          US 08/187,407
;   FILING DATE:                 27-JAN-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:          US 07/493,299
;   FILING DATE:                 14-MAR-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:          US 07/324,392
;   FILING DATE:                 14-MAR-1989
;   ATTORNEY/AGENT INFORMATION:
;   NAME:                        Carter, Charles G.
;   REGISTRATION NUMBER:         35,093
;   REFERENCE/DOCKET NUMBER:     8648.39USC1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:                   612-332-5300
;   TELEFAX:                     612-332-9081
;   INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:                      107 amino acids
;   TYPE:                        amino acid
;   TOPOLOGY:                    linear
;   MOLECULE TYPE:               protein
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US-08-888-366-22

Query Match   75.1%; Score 510.5; DB 2; Length 107;
Best Local Similarity   91.6%; Pred. No. 4.1e-43;
Matches   98; Conservative   3; Mismatches   5; Indels   1; Gaps   1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        |||||||||||||||||||||||| ||||||||:||||||||| |||||||||| ||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
        |||||||||||||:|||||:||:|||||||||| ||||||:|||||||
Db   61 RFSGSGSGRDYSFSISNPEPDIATYYCLQYDNSLFTFGSGTKLEIK 107

RESULT 9
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   CLASSIFICATION: 424
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-7

Query Match   74.7%; Score 508; DB 2; Length 106;
Best Local Similarity   88.7%; Pred. No. 7e-43;
Matches   94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        |||||||||||||| ||||||||||||||||||||| ||| |||||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        ||||||||||| | |: |||||||||||||||||||||:|||:|||
Db   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106

RESULT 10
PCT-US95-01219-7
; Sequence 7, Application PCT/US9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   PRIOR APPLICATION DATA:
;   CLASSIFICATION:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-7

Query Match   74.7%; Score 508; DB 5; Length 106;
Best Local Similarity   88.7%; Pred. No. 7e-43;
Matches   94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        |||||||||||||| ||||||||||||||||||||| ||| |||||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
        ||||||||||| | |: |||||||||||||||||||||:|||:|||
Db   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106

RESULT 11
US-08-235-838-16
; Sequence 16, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
;   APPLICANT: Wels, Winfried S.
;   APPLICANT: Hynes, Nancy E.
;   APPLICANT: Harwerth, Ina-Maria
;   APPLICANT: Groner, Bernd

Left column

;
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: USA
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-838-16

Query Match   74.7%;   Score 508; DB 1;   Length 637;
Best Local Similarity   86.4%;   Pred. No. 5.8e-42;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

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Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
           |||:||||||||||||||||||:|||||||:||||||| ||||||||:|||||||||:||
Db  164 GGGSDIQLTQSPSSLSASLGGEVTICKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||||||||:|| ||||||||||:|||||||||||||||||
Db  224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYTFGGGTKLEIK 273
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RESULT 12
US-08-465-473B-16
Sequence 16, Application US/0845473B
Patent No. 5939531
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue

Right column

CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-473B-16

Query Match   74.7%;   Score 508; DB 2;   Length 637;
Best Local Similarity   86.4%;   Pred. No. 5.8e-42;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

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Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
           |||:||||||||||||||||||:|||||||:||||||| ||||||||:|||||||||:||
Db  164 GGGSDIQLTQSPSSLSASLGGEVTICKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||||||||:|| ||||||||||:|||||||||||||||||
Db  224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYTFGGGTKLEIK 273
```

RESULT 13
US-08-235-838-11
Sequence 11, Application US/08235838
Patent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/235,838
;   FILING DATE: TBA
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/828,832
;   FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: GB 91-810079.3
;   FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Elmer, James Scott
;   REGISTRATION NUMBER: 36,129
;   REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (919)541-8614
;   TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 241 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-235-838-11

Query Match   74.0%; Score 503; DB 1; Length 241;
Best Local Similarity 86.2%; Pred. No. 5.7e-42;
Matches 94; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
        |||:||||||||||||||||| |||| :|| ||||| |:|||||||||| ||||||||| |||
Db 133 GGGSDIQLTQSPSSLSASLGGEVTTCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 192

Qy 77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
        |||||||||||||||||:|:|||||||||||||:|||| :|||||||||| |||
Db 193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYTFGGGTKLEI 241

RESULT 14
US-08-465-473B-11
Sequence 11, Application US/0846473B
Patent No. 5939531
; GENERAL INFORMATION:
;   APPLICANT: Wels, Winfried S.
;   APPLICANT: Hynes, Nancy E.
;   APPLICANT: Harwerth, Ina-Maria
;   APPLICANT: Groner, Bernd
;   APPLICANT: Hardman, No. 593951man
;   APPLICANT: Zwickl, Markus
;   TITLE OF INVENTION: Recombinant Antibodies Specific for a
;   TITLE OF INVENTION: Growth Factor Receptor
;   NUMBER OF SEQUENCES: 34
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: NOVARTIS Corporation
;   STREET: 564 Morris Avenue
;   CITY: Summit
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07901-6940
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/465,473B
;   FILING DATE: 5 June 1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/828,832
;   FILING DATE: 31-JAN-1992

; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: GB 91-810079.3
;   FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Pfeiffer, Hesna J.
;   REGISTRATION NUMBER: 22,640
;   REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (908)522 6940
;   TELEFAX: (908)522 6955
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 241 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-465-473B-11

Query Match   74.0%; Score 503; DB 2; Length 241;
Best Local Similarity 86.2%; Pred. No. 5.7e-42;
Matches 94; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
        |||:||||||||||||||||| |||| :|| ||||| |:|||||||||| ||||||||| |||
Db 133 GGGSDIQLTQSPSSLSASLGGEVTTCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 192

Qy 77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
        |||||||||||||||||:|:|||||||||||||:|||| :|||||||||| |||
Db 193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYTFGGGTKLEI 241

RESULT 15
US-08-875-811-57
Sequence 57, Application US/08875811
Patent No. 6045793
; GENERAL INFORMATION:
;   APPLICANT: Rybak, Susanna M.
;   APPLICANT: Newton, Dianne L.
;   APPLICANT: Boque, Lluis
;   APPLICANT: Wlodawer, Alexander
;   TITLE OF INVENTION: Recombinant Ribonuclease Proteins
;   NUMBER OF SEQUENCES: 64
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/875,811
;   FILING DATE: 19-FEB-1998
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US97/02588
;   FILING DATE: 19-FEB-1997
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/011,800
;   FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Faris, Susan K.
;   REGISTRATION NUMBER: 41,739
;   REFERENCE/DOCKET NUMBER: 015280-24410US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 57:

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;
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  355 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  protein
US-08-875-811-57


Query Match           73.7%;    Score 501;  DB 3;   Length 355;
Best Local Similarity  86.4%;   Pred. No. 1.4e-41;
Matches   95;  Conservative   4;  Mismatches  11;  Indels   0;  Gaps   0;

Qy      17  GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP   76
                |  ||||||||||||||||||||| |||| : ||||||||||||| ||||||||||| |||
Db     245  GGGSDIQMTQSPSSLSASLGGKVTITCKASQDIKKSIAWYQHKPGKGPRLLIHYTSTLQP  304

Qy      77  GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK          126
            ||||||||||||| :|||:||||||||||||||||| ||||||||||:|
Db     305  GIPSRFSGSGSGEEYSFSISNLEPEDIATYYCQQYDNLRTFGGGTKLELK          354


Search completed: May  7, 2002, 12:23:03
Job time: 174 sec
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OM protein - protein search, using sw model

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GenCore version 4.5

Run on: May 7, 2002, 12:20:29 ; Search time 37.68 Seconds
                                            (without alignments)
                                            254.724 Million cell updates/sec

Title:
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC............YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :   PIR.68:*
                   1: pir1:*
                   2: pir2:*
                   3: pir3:*
                   4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	589	86.6	125	2	S09365	Ig kappa chain - m
2	535	78.7	104	2	S26330	Ig kappa chain V r
3	526	77.4	104	2	S26329	Ig kappa chain V r
4	524	77.1	106	2	C33936	Ig kappa chain V r
5	490.5	72.1	129	2	S52789	Ig kappa chain V r
6	490	72.1	103	2	S26332	Ig light chain V r
7	488	71.8	97	2	PH1064	Ig kappa chain V r
8	476	70.0	94	2	E33730	Ig light chain V r
9	471.5	69.3	107	2	PL0270	Ig kappa chain V r
10	465.5	68.5	107	2	PL0272	Ig kappa chain V r
11	464.5	68.3	107	2	PL0269	Ig kappa chain V r
12	464.5	68.3	107	2	PL0271	Ig kappa chain V r
13	453.5	66.7	127	2	S40367	Ig kappa chain V-J
14	453.5	66.7	132	2	S40334	Ig kappa chain - h
15	445.5	65.5	139	2	S40365	Ig kappa chain - h
16	444.5	65.4	129	2	S40366	Ig kappa chain - h
17	443.5	65.2	125	2	S40317	Ig kappa chain V-J
18	442.5	65.1	131	2	S40333	Ig kappa chain V-J
19	442.5	65.1	129	2	S40352	Ig kappa chain pre
20	441.5	64.9	129	2	K1HUWK	Ig kappa chain pre
21	439.5	64.6	94	2	PH1063	Ig light chain V-J
22	439	64.6	124	2	S40336	Ig kappa chain V-J
23	438.5	64.5	123	2	S40331	Ig kappa chain - h
24	437.5	64.4	117	2	S42263	Ig kappa chain V r
25	437.5	64.4	122	2	A29380	Ig kappa chain V r
26	437.5	64.3	127	2	S52447	Ig kappa chain V r
27	436.5	64.3	135	2	S24320	Ig kappa chain pre
28	436.5	64.2	128	2	PL0101	Ig kappa chain pre
29	435.5	64.0	127	2	S04574	Ig kappa chain V r
30	435.5	64.0	127	2	S11240	Ig kappa chain V r
31	434.5	63.9	141	2	A49134	Ig kappa chain V-I
32	433.5	63.8	126	2	A34904	Ig kappa chain pre
33	433.5	63.8	234	2	S14237	Ig kappa chain pre
34	432	63.5	117	2	S43528	Ig kappa chain V r
35	430.5	63.3	127	2	PH1224	Ig kappa chain pre
36	428.5	63.0	125	2	S40314	Ig kappa chain - h
37	427.5	62.9	129	2	S52792	Ig kappa chain pre
38	426.5	62.7	125	2	S40350	Ig kappa chain V-J
39	425.5	62.6	125	2	S40349	Ig kappa chain - h
40	425.5	62.6	128	2	KVMST1	Ig kappa chain V-J
41	422.5	62.1	124	2	S40348	Ig kappa chain - h
42	419.5	61.7	122	2	S40314	Ig kappa chain - h
43	419.5	61.7	124	2	S03521	Ig kappa chain pre
44	418	61.5	127	2	A23986	Ig kappa chain pre
45	416.5	61.2	85	2	F36025	Ig light chain V r

ALIGNMENTS

RESULT 1

S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene s
Nucleic Acids Res. 17, 9797-9809, 1989
A;Reference number: S09365; MUID:90098844
A;Accession: S09365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match   86.6%; Score 589; DB 2; Length 125;
Best Local Similarity   90.6%; Pred. No. 4.8e-44;
Matches 115; Conservative   2; Mismatches   6; Indels   4; Gaps   2;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYMAWYQHKP 60
           ||||||||||||||||||| |||||||||||||||||||||| |||||||:||||||||
Db   1 MRPSIQFLGLLLFWLHG--DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 57

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW-TFGG 119
           |||||||||| ||||||||||||||||| || ||||||||||||||||||||||| ||||
Db   58 GKGPRLLIHYTSTLQPGIPSRFSGSGSGSDYSFSISNLGPEDIATYCLQYDNLLRTFGG 117

Qy   120 GTKLEIK 126
           |||||||
Db   118 GTKLEIK 124

RESULT 2

S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S. E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g523316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   78.7%;   Score 535; DB 2; Length 104;
Best Local Similarity 95.2%;   Pred. No. 1.8e-39;
Matches 99;   Conservative   2;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS   80
          ||||||||||||||||||||||||||||:|:||||||||||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS   60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
          ||||||||||||||||||||||||||||:|||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104

RESULT 3
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   77.4%;   Score 526; DB 2; Length 104;
Best Local Similarity 94.2%;   Pred. No. 1.1e-38;
Matches 98;   Conservative   3;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS   80
          ||||||||||||||||||||||||||:||||||||||||||||||||||||||:|||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS   60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
          ||||||||||||||||||||||||||||:|||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104

RESULT 4
C33936
Ig kappa chain V region (VM13) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   77.1%;   Score 524; DB 2; Length 106;
Best Local Similarity 91.5%;   Pred. No. 1.6e-38;
Matches 97;   Conservative   6;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS   80
          ||||||||||||||||||||||||||||:|:||||||||||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS   60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          ||||||||||||||:|||||||||||||||:||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106

RESULT 5
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Der
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myelo
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   72.1%;   Score 490.5; DB 2; Length 129;
Best Local Similarity 72.4%;   Pred. No. 1.5e-35;
Matches 92;   Conservative 15;   Mismatches 19;   Indels   1;   Gaps   1;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP   60
          | |||||| ||||| |||||||||||||||||||||:||||||||||| |||: ||| ||
Db   3 MRVPAQLLGLILWLSGARCDIQMTQSPSSLSASVGDRVTIICQASQDISNYLNWYQQKP   62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
          || ||||||||| :|||||||||||||||:|||:::|||||| ||| ||:||||| ||||
Db   63 GKAPKLLIHAASSLETGVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQYDNLPLTFGG 122

Qy   120 GTKLEIK 126
          |||:|:||
Db   123 GTKVEIK 129

RESULT 6
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

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Query Match
Best Local Similarity    72.1%;    Score 490;   DB 2;   Length 103;
Matches    90;   Conservative    87.4%;   Pred. No. 1.3e-35;   Mismatches    7;   Indels    6;   Gaps    0;

Qy    21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIS  80
          ||||||||||||||||||||| ||||| ||| |||:||||||||  |||||:||||||||||
Db     1  DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIS  60

Qy    81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKL  123
          ||||| || |||::|::|| ||||||||:||||| ||||||||
Db    61  RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL  103
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RESULT 7
PH1064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
J. Exp. Med. 176, 761-779, 1992
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A;Reference number: PH0971; MUID:92381444
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin V region; immunoglobulin homology

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Query Match
Best Local Similarity    71.8%;   Score 488;   DB 2;   Length 97;
Matches    91;   Conservative    93.8%;   Pred. No. 1.9e-35;   Mismatches    3;   Indels    0;   Gaps    0;

Qy    21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIS  80
          |||||||||||||||||||| |||||||||||||:||||||||| |||||||||||||||
Db     1  DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIS  60

Qy    81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTF  117
          |||||||||||| |:||||||||||||||:|||||||
Db    61  RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF  97
```

RESULT 8
E3730
Ig kappa chain V region (9.42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: E3730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unl
A;Reference number: A33730; MUID:89367325
A;Accession: E3730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: GB:M26000; NID:g197119; PIDN:AAA38916.1; PID:g197120
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin V region; immunoglobulin homology

```
Query Match
Best Local Similarity    70.0%;   Score 476;   DB 2;   Length 94;
Matches    89;   Conservative    94.7%;   Pred. No. 1.9e-34;   Mismatches    3;   Indels    0;   Gaps    0;

Qy    21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKPRLLIHYTSTLQPGIS  80
          |||||||||||||||||||||||||||||||||:|||||||| |||||||||||||||
Db     1  DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIS  60
```

```
Qy    81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL  114
          |||||||||||| |:||||||||||||||:||||
Db    61  RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL  94
```

RESULT 9
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

```
Query Match
Best Local Similarity    69.3%;   Score 471.5;   DB 2;   Length 107;
Matches    92;   Conservative    86.0%;   Pred. No. 5.4e-34;   Mismatches    9;   Indels    1;   Gaps    1;

Qy    21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIS  80
          |||||||| ||||||| ||||| | |||||:|||||||||  |||||  ||||| |||||
Db     1  DIQMTQSPCSLSASLGDKVTIICRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIS  60

Qy    81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  126
          |||||||||||| |:||||||||||||||:|||| ::| |||||||||
Db    61  RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYFGSGTKLEIK  107
```

RESULT 10
PL0272
Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

```
Query Match
Best Local Similarity    68.5%;   Score 465.5;   DB 2;   Length 107;
Matches    91;   Conservative    85.0%;   Pred. No. 1.8e-33;   Mismatches    10;   Indels    1;   Gaps    1;

Qy    21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIS  80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIS  60
```

RESULT 11
PL0269

```
Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS   80
             |||||||| ||||||  |||  |:|||||:|| |||||||||| ||||||:|||:|||||
Db    1  DIQMTQSPCSLSASLGDKVIITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS   60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK   126
             ||||||||||||  |||:||||||||||||| ::|||  ||||||
Db   61  RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK   107
```

Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0269
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   68.38;   Score 464.5;   DB 2;   Length 107;
Best Local Similarity   85.0%;   Pred. No. 2.2e-33;
Matches   91;   Conservative   4;   Mismatches   11;   Indels   1;   Gaps   1;

RESULT 12
PL0271

```
Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS   80
             ||||||||||||||  |||  |:|||||:|| |||||||||| ||||||:|||:|||||
Db    1  DIQMTQSPSSLSASLGDKVIIACRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS   60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK   126
             ||||||||||||  |||:||||||||||||| ::|||  ||||||
Db   61  RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK   107
```

Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   68.38;   Score 464.5;   DB 2;   Length 107;

Best Local Similarity   85.0%;   Pred. No. 2.2e-33;
Matches   91;   Conservative   4;   Mismatches   11;   Indels   1;   Gaps   1;

```
Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS   80
             |||||||| |||||||  |||  |:|||||:|| |||||||||| ||||||:|||:|||||
Db    1  DIQMTQSPCSLSASLGDKVIITCRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS   60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK   126
             ||||||||||||  |||:||||||||||||| ::|||  ||||||
Db   61  RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK   107
```

RESULT 13
S40367

Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40367
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match   66.7%;   Score 453.5;   DB 2;   Length 127;
Best Local Similarity   68.9%;   Pred. No. 2.3e-32;
Matches   84;   Conservative   16;   Mismatches   21;   Indels   1;   Gaps   1;

```
Qy    6  QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR   65
          | |||||:|| :|| |||||||||||||||:| :|||||  :|||: || |||||:||| :
Db    3  QLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQRKPGKAPK   62

Qy   66  LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE   124
          |||: :|| | ||:|||||||||| |:: :|:||:|||:||||||| :  |:|||  ||:|
Db   63  LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKVE   122

Qy  125  IK   126
          ||
Db  123  IK   124
```

RESULT 14
S40334

Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match   65.5%;   Score 445.5;   DB 2;   Length 132;
Best Local Similarity   64.6%;   Pred. No. 1.1e-31;
Matches   82;   Conservative   21;   Mismatches   23;   Indels   1;   Gaps   1;

```
RESULT 15
S40365
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40365
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin ch1 genes and their hypermutation.
A;Reference number: S40312; MUID:9408089l
A;Accession: S40365
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:X72475; NID:g441418; PIDN:CAA51143.1; PID:g441419
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>


Query Match          65.4%;   Score 444.5;  DB 2;   Length 139;
Best Local Similarity   68.9%;   Pred. No. 1.5e-31;
Matches   84;   Conservative   14;   Mismatches   23;   Indels   1;  Gaps   1;


Qy      6  QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR  65
              |||||| || |||||||||||||||||||||||||:||| |: ||||||||||||||
Db      1  QLLGLLLLWLSGATCDIQMTQSPSSLSASVGDRVTITCQATQDIGNYLNWYQHKPGKAPN  60

Qy     66  LLIHYTSALQPGTPSRFSGSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLE  124
              || :   |: |:|||||||| ||| ::|:||||||||| ::|||||||||-|||||:
Db     61  LLIYDASNLETGVPSRFSGRGSGTHFTFTISSLQPEDIATYYCQQYGNLPTFGPGTKVH  120

Qy    125  IK  126
              ||
Db    121  IK  122
```

Search completed: May 7, 2002, 12:23:47
Job time: 198 sec

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                          GenCore version 4.5
          OM protein - protein search, using sw model
          Copyright (c) 1993 - 2000 Compugen Ltd.
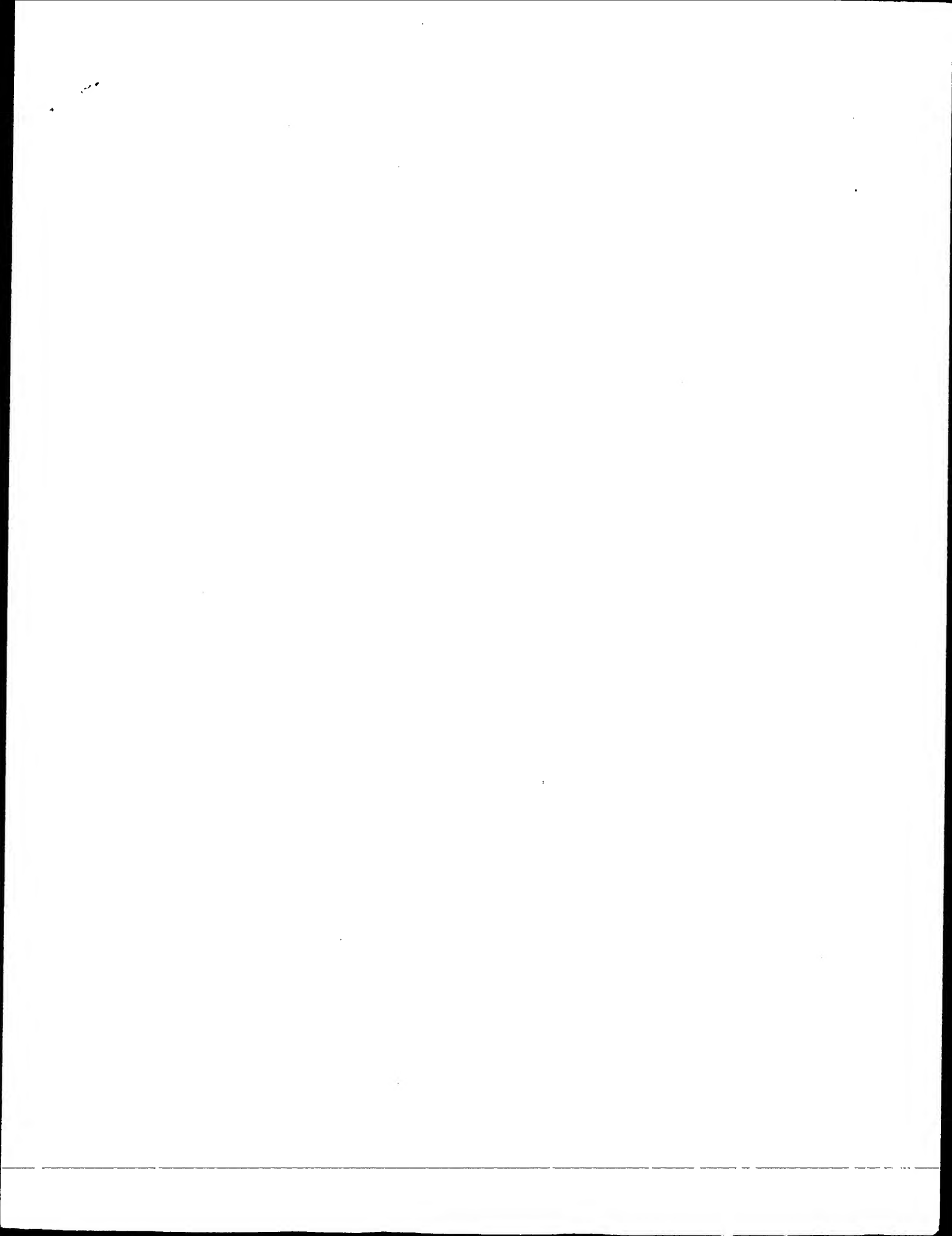
Run on:   May 7, 2002, 12:23:09 ; Search time 21.92 Seconds
                                  (without alignments)
                                  210.756 Million cell updates/sec

Title:        US-09-155-739-2
Perfect score: 680
Sequence:   1 MRPSIQFLGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:    100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SwissProt_39:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	441.5	64.9	129	1	KV1W_HUMAN	P04431 homo sapiens
2	425.5	62.6	128	1	KV5E_MOUSE	P01637 mus musculu
3	412.5	60.7	129	1	KV1X_HUMAN	P04432 homo sapiens
4	402	59.1	117	1	KV1J_HUMAN	P01602 homo sapien
5	400	58.8	115	1	KV5F_MOUSE	P01638 mus musculu
6	397.5	58.8	108	1	KV1B_HUMAN	P01594 homo sapien
7	395.5	58.2	108	1	KV1O_HUMAN	P01607 homo sapien
8	392.5	57.7	108	1	KV1P_HUMAN	P01608 homo sapien
9	389.5	57.3	108	1	KV1Y_HUMAN	P01613 homo sapien
10	380.5	56.0	108	1	KV1A_HUMAN	P01593 homo sapien
11	379.5	55.8	108	1	KV1M_HUMAN	P01605 homo sapien
12	378.5	55.7	130	1	KV5G_MOUSE	P01639 mus musculu
13	378.5	55.7	133	1	KV4B_HUMAN	P06313 homo sapien
14	378	55.6	117	1	KV1I_HUMAN	P01601 homo sapien
15	377.5	55.5	108	1	KV5J_MOUSE	P01643 mus musculu
16	377	55.4	108	1	KV1D_HUMAN	P01596 homo sapien
17	375	55.1	134	1	KV4C_HUMAN	P06314 homo sapien
18	374.5	55.1	108	1	KV5O_MOUSE	P01648 mus musculu
19	373.5	54.9	108	1	KV1Q_HUMAN	P01609 homo sapien
20	373.5	54.9	108	1	KV5N_MOUSE	P01647 mus musculu
21	371.5	54.6	108	1	KV5K_MOUSE	P01644 mus musculu
22	369.5	54.3	108	1	KV5M_MOUSE	P01646 mus musculu
23	368.5	54.2	108	1	KV5L_MOUSE	P01645 mus musculu
24	366.5	53.9	108	1	KV1R_HUMAN	P01610 homo sapien
25	362.5	53.3	108	1	KV1C_HUMAN	P01595 homo sapien
26	360.5	53.0	108	1	KV1H_HUMAN	P01600 homo sapien
27	359.5	52.9	108	1	KV1N_HUMAN	P01606 homo sapien
28	357.5	52.6	108	1	KV1E_HUMAN	P01597 homo sapien
29	357.5	52.6	108	1	KV1F_HUMAN	P04430 homo sapien
30	355.5	52.3	108	1	KV1S_HUMAN	P01598 homo sapien
31	354.5	52.1	108	1	KV1F_HUMAN	P01611 homo sapien
32	353.5	52.0	115	1	KV5C_MOUSE	P01635 mus musculu
33	352.5	51.8	108	1	KV1K_HUMAN	P01603 homo sapien
34	350.5	51.5	108	1	KV1L_HUMAN	P01604 homo sapien
35	349.5	51.4	108	1	KV5U_MOUSE	P04946 mus musculu
36	347	51.0	129	1	KV3H_HUMAN	P04207 homo sapien
37	347	51.0	129	1	KV3M_HUMAN	P18136 homo sapien
38	343	50.4	117	1	KV5H_MOUSE	P01641 mus musculu
39	341.5	50.2	108	1	KV1G_HUMAN	P01599 homo sapien
40	341	50.1	110	1	KV3P_MOUSE	P01668 mus musculu
41	339.5	49.9	108	1	KV5T_MOUSE	P01653 homo sapien
42	338	49.7	129	1	KV3L_HUMAN	P18135 homo sapien
43	337.5	49.6	131	1	KV3I_MOUSE	P01661 mus musculu
44	335.5	49.3	108	1	KV5P_MOUSE	P01649 mus musculu
45	335.5	49.3	108	1	KV5Q_MOUSE	P01650 mus musculu

ALIGNMENTS

```
RESULT 1
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as  long as its content is  in  no  way
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; K1HUWK.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      120    129       FRAMEWORK 4.
FT   NON_TER       1      1
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

Query Match             64.9%;  Score 441.5;  DB 1;  Length 129;
Best Local Similarity   66.9%;  Pred. No. 5.2e-38;
Matches   85;  Conservative  15;  Mismatches  26;  Indels  1;  Gaps  1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         || |||||||||||||||| |||||||||||||||||| | ||| ||: |||||| |||
```

```
Db      3 MRVPAQLGLLLLWLLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKP

Qy     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
          ||.|:||:|  |:|||||| |:||||||||| ||.|:|:||||||||||||| ||||||||
Db     63 GKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQ 122

Qy    120 GTKLEIK 126
          ||:||||
Db    123 GTRLEIK 129
```

RESULT 2

```
ID   KV5E_MOUSE    STANDARD;    PRT;   128 AA.
AC   P01637;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION T1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81052342; PubMed=6776411;
RA   Altenburger W., Steinmetz M., Zachau H.G.;
RT   "Functional and non-functional joining in immunoglobulin light chain
RT   genes of a mouse myeloma.";
RL   Nature 287:603-607(1980).
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DR   EMBL; V00772; CAA24150.1; -.
DR   PIR; A01920; KVMST1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    128       IG KAPPA CHAIN V-V REGION T1.
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       77    108       FRAMEWORK 3.
FT   DOMAIN      109    117       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      118    127       FRAMEWORK 4.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     128    128
SQ   SEQUENCE   128 AA;   14385 MW;   AFA5563D31BB7E05 CRC64;
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Query Match     62.6%;   Score 425.5;  DB 1;  Length 128;
Best Local Similarity   62.2%;   Pred. No. 2.2e-36;
Matches   79;  Conservative   18;  Mismatches   29;  Indels   1;  Gaps   1;
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Qy     1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         ||.| ||| || :|: .|||||||||||||||||| |.||| | :|| |.|.| |||.||
Db     1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTISCKASQDINSYLSWFQQKP 60

Qy    61 GKRPRLLIHYTSALQPGIPSRFSGSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
         ||||.:|:|.||  ||||  |||||||  :||||:|||||||||| |.| :|| ||| ||||
Db    61 GKSPKTLLYRANRLVDGVPSRFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGA 120

Qy   120 GTKLEIK 126
         |||:| |
Db   120 GTKVDNK 129
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RESULT 4
KVIJ_HUMAN

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Db    121 GTKLEIK 127
```

RESULT 3

```
ID   KVIX_HUMAN    STANDARD;    PRT;   129 AA.
AC   P04432;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION DAUDI PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
```

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DR   EMBL; X00966; CAA25478.1; ALT_TERM.
DR   PIR; A01884; KIHUDI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION DAUDI.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      120    129       FRAMEWORK 4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;   14235 MW;   CAF076BC7E5574C8 CRC64;
```

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Query Match     60.7%;   Score 412.5;  DB 1;  Length 129;
Best Local Similarity   61.4%;   Pred. No. 4.5e-35;
Matches   78;  Conservative   19;  Mismatches   29;  Indels   1;  Gaps   1;
```

```
Qy     1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         ||.| ||| ||:|: ||||||||||||||||||| |.|||.| :||.|.|.|.|||.||
Db     3 MRVPAQLGLLLLWLRRVRCDIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKP 62

Qy    61 GKRPRLLIHYTSALQPGIPSRFSGSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
         |||| :|:|  |:|||||| |:||||||||| :|| |||.|||||||||||| |:||||||
Db    63 GKAPLLLIYAVSNLQVGVPSRFSGSGSGCAEFTLTISSLQPEDFATYYCQQNNFSFGTFGG 122

Qy   120 GTKLEIK 126
         |||:|||
Db   123 GTRLEIK 129
```

RESULT 4
KVIJ_HUMAN

ID   KV1I_HUMAN   STANDARD;   PRT;   117 AA.
AC   P01602;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION HK102 PRECURSOR (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; J00245; AAA59087.1; -.
DR   EMBL; Z00001; CAA77292.1; -.
DR   PIR; A01882; KIHU12.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   22
FT   CHAIN   23   >117   IG KAPPA CHAIN V-I REGION HK102.
FT   DOMAIN   23   45   FRAMEWORK 1.
FT   DOMAIN   46   56   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   57   71   FRAMEWORK 2.
FT   DOMAIN   72   78   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   79   110   FRAMEWORK 3.
FT   DOMAIN   111   >117   COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID   45   110   BY SIMILARITY.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 12768 MW; A01DF3A40AF1A49B CRC64;

Query Match   59.1%; Score 402; DB 1; Length 117;
Best Local Similarity   63.7%; Pred. No. 4.7e-34;
Matches   72; Conservative 21; Mismatches 20; Indels   0; Gaps   0;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
              || ||||||||||||| |||||||||||||||||||| ||||| |: ||||||| |:||
Db   3 MRVPAQLLGLLLLWLPGAKCDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGGSGRDYSFNISNLEPEDIATYYCLQYDN 113
              |: ||||||: |:|:|||||||||| ||| ::| ||:||||: :||:|||||||
Db   63 GKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNS 115

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RESULT 5
KV5F_MOUSE
ID   KV5F_MOUSE   STANDARD;   PRT;   115 AA.
AC   P01638;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION L6 PRECURSOR (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
DR   PIR; A01921; KVMSL6.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   >115   IG KAPPA CHAIN V-V REGION L6.
FT   DOMAIN   21   43   FRAMEWORK 1.
FT   DOMAIN   44   54   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   55   69   FRAMEWORK 2.
FT   DOMAIN   70   76   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   77   108   FRAMEWORK 3.
FT   DOMAIN   109   >115   COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID   43   108   BY SIMILARITY.
FT   NON_TER   115   115
SQ   SEQUENCE   115 AA; 12986 MW; BA852C58F328E1C3 CRC64;

Query Match   58.8%; Score 400; DB 1; Length 115;
Best Local Similarity   65.2%; Pred. No. 7.4e-34;
Matches   73; Conservative 15; Mismatches 24; Indels   0; Gaps   0;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
              || |||||||||||| |||||||||||||| ||||: |||||||||::|| || ||||
Db   1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVITCKASQDINSYLSWFQQKP 60

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGGSGRDYSFNISNLEPEDIATYYCLQYD 112
              |: ||||||:: |:|||||||||||||||| ||: |||| |: ||| |: ||||
Db   61 GKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYD 112

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RESULT 6
KV1B_HUMAN
ID   KV1B_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77024433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC   MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC   REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; KIHUAU.

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RESULT 7
ID   KV10_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION REI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei.); Isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC       MARKER.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
DR   PIR; A01873; KIHURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig1; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

Query Match             58.5%;
Best Local Similarity   70.1%;
Matches   75;  Conservative   14;  Mismatches   17;  Indels    1;  Gaps    1;

        Score 397.5;  DB 1;  Length 108;  Pred. No. 1.2e-33;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDIINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
         |||||||||||||| :|| :|||| :|||| |  ||||| ||    |||:||  |   :||
Db    1  DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS  60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  126
         |||| ||| :|| ||| ||||||||||| ||| |  |||| ||| |||
Db   61  RFSGGGSGAHFTFISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK  107
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RESULT 8
ID   KV1P_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION ROY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RT   (In) Franck F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
RN   [2]
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC       MARKER.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
DR   PIR; A01874; KIHURY.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig1; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   STRAND        4      8
FT   TURN         10     13
FT   STRAND       15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   TURN         45     49
FT   STRAND       50     52
FT   TURN         53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   STRAND       68     69
FT   HELIX        70     75
FT   STRAND       80     82
FT   STRAND       85     90
FT   TURN         98     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

Query Match             58.2%;
Best Local Similarity   71.7%;
Matches   76;  Conservative   13;  Mismatches   16;  Indels    1;  Gaps    1;

        Score 395.5;  DB 1;  Length 108;  Pred. No. 2e-33;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDIINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
         |||||||||||||| :|| :|||| :|||| |||||| :|||||:||   |   ||:||
Db    1  DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS  60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  125
         ||||||||:|| | ||| |||||||||| || :|  |||| ||| |
Db   61  RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI  106
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DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11782 MW;   F5ACEDE5A313DF3A CRC64;

  Query Match     Best Local Similarity   57.7%;   Score 392.5;  DB 1;  Length 108;
  Matches    73;   Conservative    18;   Pred. No. 4e-33;   Mismatches   15;   Indels    1;   Gaps    1;

Qy     21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
           ||||||||||||||.|..|||||  ||||      || ||||.| |.||   |.| | .||
Db      1  DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNNYQQKPGKAPKLLIYDASKLEAGVPS  60

Qy     81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  126
           |||||||| | | || | ||||||||||| | ||| |||||||   |
Db     61  RFSGSGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK  107


RESULT 9

ID   KV1Y_HUMAN   STANDARD;   PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7793911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
DR   InterPro; IPR003006; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   CONFLICT     30     31       TN -> SD (IN REF. 2).
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11737 MW;   D9D941B3F0FAE697 CRC64;

  Query Match     Best Local Similarity   57.3%;   Score 389.5;  DB 1;  Length 108;
  Matches    72;   Conservative    18;   Pred. No. 8e-33;   Mismatches   16;   Indels    1;   Gaps    1;

Qy     21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
           ||||||||||||||.|..|||||  |||||.| | | ||  | ||  || | |.| |.||
Db      1  DIQMTQSPSSLSASVGDRVTITCRASQDINNYVNWFQQRPGQAPKVLIYGASILETGVPS  60

Qy     81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  126
           |||||||| | | || | |||||||||||| | |  |||||||  ||
Db     61  RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK  107


RESULT 10

ID   KV1A_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; KIHUAG.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11992 MW;   E3B3B246C18F0C4F CRC64;

  Query Match     Best Local Similarity   56.0%;   Score 380.5;  DB 1;  Length 108;
  Matches    74;   Conservative    12;   Pred. No. 6.5e-32;   Mismatches   20;   Indels    1;   Gaps    1;

Qy     21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
           ||||||||||||||.|..|||||  |||||.|.|.|||     |||   |.| | .|.||
Db      1  DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKAPKILLIYDASNLETGVPS  60

Qy     81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK  126
           ||||||.|.| | || | |||||||||||| | |  ||| |||||||
Db     61  RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK  107


RESULT 11
```

```
KV1M_HUMAN
ID   KV1M_HUMAN    STANDARD;    PRT;    108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION LAY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; KIHULY.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN     1     23    FRAMEWORK 1.
FT   DOMAIN    24     34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN    35     49    FRAMEWORK 2.
FT   DOMAIN    50     56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN    57     88    FRAMEWORK 3.
FT   DOMAIN    89     97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN    98    107    FRAMEWORK 4.
FT   DISULFID  23     88    BY SIMILARITY.
FT   NON_TER  108    108
SQ   SEQUENCE   108 AA;   11834 MW;   739993A95431434A CRC64;
```

```
RESULT 12
KV5G_MOUSE
ID   KV5G_MOUSE    STANDARD;    PRT;    130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION MOPC 41 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=79221900; PubMed=111146;
RA   Seidman J.G., Max E.E., Leder P.;
RT   "A kappa-immunoglobulin gene is formed by site-specific recombination
RT   without further somatic mutation.";
RL   Nature 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE=77149916; PubMed=403522;
RA   Burstein Y., Schechter I.;
RT   "Amino acid sequence of the NH2-terminal extra piece segments of the
RT   precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT   chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE=67056897; PubMed=4162931;
RA   Gray W.R., Dreyer W.J., Hood L.;
RT   "Mechanism of antibody synthesis: size differences between mouse
RT   kappa chains.";
RL   Science 155:465-467(1967).
CC   -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
CC       SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01922; KVMSM4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal; Bence-Jones protein.
FT   SIGNAL     1     22
FT   CHAIN     23    130
FT   DOMAIN    23     45    FRAMEWORK 1.
FT   DOMAIN    46     56    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN    57     71    FRAMEWORK 2.
FT   DOMAIN    72     78    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN    79    110    FRAMEWORK 3.
FT   DOMAIN   111    119    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   120    129    FRAMEWORK 4.
FT   DISULFID  45    110    BY SIMILARITY.
FT   VARIANT    1      2    MISSING (IN 25% OF THE MOLECULES).
FT   NON_TER  130    130
SQ   SEQUENCE   130 AA;   14311 MW;   5EFE0FE71D5F1BEC CRC64;
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Query Match             55.8%;  Score 379.5;  DB 1;  Length 108;
Best Local Similarity   65.7%;  Pred. No. 8.2e-32;
Matches   71;  Conservative   17;  Mismatches   17;  Indels    3;  Gaps    2;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         |||||||||||:|| ::|||||| ::|:|:| |||  |||:|||||| : |:||
Db    1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNAVLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
         |||||:||| ::|||||||||||||| |:||:|||  ||||||||||:|
Db   61 RFSGSGSGTDFFTISSLQPEDIATYYCQQYNN-WPPTFGQGTKVEVK 107
```

```
Query Match             55.7%;  Score 378.5;  DB 1;  Length 130;
Best Local Similarity   59.1%;  Pred. No. 1.3e-31;
Matches   75;  Conservative   13;  Mismatches   38;  Indels    1;  Gaps    1;

Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         ||  || |  |||||||||||||||||||:|| :|||||||| ::|:|:|||| |||
Db    3 MRAPAQIFGFLLLLFQGTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGG 119
         |||||||||| | :|| ||||||||||||||||  | |||||:|| : ||||| :|||||
Db   63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYCLQYASSPWTFGG 122

Qy  120 GTKLEIK 126
         |||||||
Db  123 GTKLEIK 129
```

```
RESULT 13
KV4B_HUMAN
ID   KV4B_HUMAN    STANDARD;    PRT;    133 AA.
AC   P06313;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041853; PubMed=2997712;
```

RA   Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA   Zachau H.G.;
RT   "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT   single germline gene.";
RL   Nucleic Acids Res. 13:6515-6529(1985).
DR   EMBL; Z00022; CAA77317.1; -.
DR   PIR; A01904; K4HUJI.
DR   HSSP; P01789; 2MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   133   IG KAPPA CHAIN V-IV REGION JI.
FT   DOMAIN   21   43   FRAMEWORK 1.
FT   DOMAIN   44   60   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   61   75   FRAMEWORK 2.
FT   DOMAIN   76   82   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   83   114   FRAMEWORK 3.
FT   DOMAIN   115   122   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   123   132   FRAMEWORK 4.
FT   DISULFID   43   114   BY SIMILARITY.
FT   NON_TER   133   133
SQ   SEQUENCE   133 AA; 14632 MW; 5FB395306744AF4 CRC64;

Query Match   55.7%; Score 378.5; DB 1; Length 133;
Best Local Similarity   57.9%;
Matches   73; Conservative   20; Mismatches   26; Indels   7; Gaps   3;

Qy   7 FLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI-----NK-YMAWYQHKP 60
         : ||| ||| ||:||||||||||||||||||||||||||||| || :||||||||
Db   8 FISLLL-WISGAYGDIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQQKP 66

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
         |||| | :||:|| | |:|||||||||||||| | ::||:|||||:| :||||| |
Db   67 GQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDIPIPTFGGG 126

Qy 121 TKLEIK 126
         ||:|||
Db 127 TKVEIK 132

RESULT 14
ID   KV1I_HUMAN   STANDARD;   PRT;   117 AA.
AC   P01601;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION HK101 PRECURSOR (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
RN   [2]

RP   SEQUENCE FROM N.A.
RX   MEDLINE=83129397; PubMed=6402305;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Evolution of immunoglobulin V genes: evidence indicating that
RT   recently duplicated human V kappa sequences have diverged by gene
RT   conversion.";
RL   Cell 32:181-189(1983).
DR   EMBL; K01322; AAA58930.1; -.
DR   EMBL; K01324; AAA58932.1; -.
DR   EMBL; V00558; CAA23824.1; -.
DR   PIR; A01881; K1HUI1.
DR   PIR; A21056; A21056.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   22
FT   CHAIN   23   >117   IG KAPPA CHAIN V-I REGION HK101.
FT   DOMAIN   23   45   FRAMEWORK 1.
FT   DOMAIN   46   56   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   57   71   FRAMEWORK 2.
FT   DOMAIN   72   78   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   79   110   FRAMEWORK 3.
FT   DOMAIN   111   >117   COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID   45   110   BY SIMILARITY.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 12799 MW; D7D0FF3718CEF587 CRC64;

Query Match   55.6%; Score 378; DB 1; Length 117;
Best Local Similarity   62.8%;
Matches   71; Conservative   17; Mismatches   25; Indels   0; Gaps   0;

Qy   1 MRSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         | | |||||||||||||||||||||||||||||:| |||||| : :||||||| ||
Db   3 MRVLAQLGLLLLCFPPGARCDIQMTQSPSSLSASVGDRVTITCRARQGISSWLAWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
         ::||| :|||||| ::||||||||||| | ||||||| : :|||||:| |::
Db   63 EKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNS 115

RESULT 15
ID   KV5J_MOUSE   STANDARD;   PRT;   108 AA.
AC   P01643;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76091934; PubMed=812696;
RA   Schiff C., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the light chain.";
RL   Eur. J. Biochem. 59:525-537(1975).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

```
DR   PIR; A01926; KVMS73.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    108       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;   11819 MW;  2AD29D92A72AA0A3 CRC64;
```

```
Query Match             55.5%;    Score 377.5;   DB 1;    Length 108;
Best Local Similarity   67.3%;    Pred. No. 1.3e-31;
Matches    72;    Conservative   12;   Mismatches   22;    Indels    1;    Gaps    1;


Qy    21   DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS    80
           ||||||:  |||||||   :||||| | ||    |   :|||:||:|:  :|:|
Db     1   DIQMTQTTSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIYTSSLHSGVPS    60

Qy    81   RFSGSGSGRDYSFNISNLEPEDIATYCLQYDNL-WTFGGGTKLEIK   126
           ||||||||  | |:|:|:|||||||| | |||||||||||||
Db    61   RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIK   107
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Search completed: May 7, 2002, 12:32:34
Job time: 565 sec

OM protein - protein search, using sw model

```
            GenCore version 4.5
            Copyright (c) 1993 - 2000 Compugen Ltd.
```

Run on: May 7, 2002, 12:21:14 ; Search time 67.26 Seconds
                                        (without alignments)
                                        274.016 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC..............YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5
Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 0

Post-processing: Minimum Match 0%
              Maximum Match 100%
              Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   SPTREMBL_17:*
              1: sp_archea:*
              2: sp_bacteria:*
              3: sp_fungi:*
              4: sp_human:*
              5: sp_invertebrate:*
              6: sp_mammal:*
              7: sp_mhc:*
              8: sp_organelle:*
              9: sp_phage:*
             10: sp_plant:*
             11: sp_rodent:*
             12: sp_virus:*
             13: sp_vertebrate:*
             14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	389.5	57.3	108	4	Q9UL77	Q9ul77 homo sapien
2	380.5	56.0	214	11	Q9R1A5	Q9r1a5 mus musculu
3	378.5	55.7	108	4	Q9UL70	Q9ul70 homo sapien
4	372.5	54.8	107	11	Q9JL84	Q9jl84 mus musculu
5	362	53.2	107	4	Q9UL81	Q9ul81 homo sapien
6	346.5	51.0	108	4	Q9UL79	Q9ul79 homo sapien
7	341.5	50.2	298	11	Q9QYF0	Q9qyf0 mus musculu
8	319	46.9	109	4	Q9UL78	Q9ul78 homo sapien
9	317.5	46.7	238	11	Q99M37	Q99m37 mus musculu
10	310	45.6	109	4	Q9UL85	Q9ul85 homo sapien
11	308	45.3	109	4	Q9UL86	Q9ul86 homo sapien
12	305.5	44.9	108	4	Q9UL83	Q9ul83 homo sapien
13	299	44.0	106	9	Q9U410	Q9u410 schistosoma
14	295.5	43.5	107	11	Q9ERZ9	Q9erz9 mus musculu
15	292.5	43.0	101	11	Q9JL78	Q9jl78 mus musculu
16	291.5	42.9	97	11	Q9JL76	Q9jl76 mus musculu
17	289.5	42.6	103	11	Q9JL80	Q9jl80 mus musculu
18	288.5	42.4	99	11	Q9JL74	Q9jl74 mus musculu
19	281.5	41.4	114	4	Q9UL80	Q9ul80 homo sapien
20	262	38.5	104	11	Q9JL82	Q9jl82 mus musculu
21	252.5	37.1	109	6	Q9N0W5	Q9n0w5 oryctolagus
22	209	30.7	107	4	Q9NSD6	Q9nsd6 homo sapien
23	204.5	30.1	107	4	Q9UL82	Q9ul82 homo sapien
24	193.5	28.5	130	4	Q9NP29	Q9np29 homo sapien
25	188.5	27.7	235	11	Q99M11	Q99m11 mus musculu
26	185	27.2	109	11	Q9ET13	Q9et13 mus musculu
27	150	22.1	337	13	Q91B02	Q91b02 sphoeroides
28	140.5	20.7	93	4	Q9UL76	Q9ul76 homo sapien
29	140	20.6	135	4	Q9H524	Q9h524 homo sapien
30	129	19.0	100	6	O77624	o77624 bos taurus
31	124	18.2	169	4	Q9Y2N4	Q9y2n4 homo sapien
32	119	17.5	509	11	Q9QW15	Q9qw15 rattus norv
33	119	17.5	509	11	P97710	p97710 rattus norv
34	118.5	17.4	342	13	Q91B00	Q91b00 sphoeroides
35	117	17.2	509	11	Q90X57	Q90x57 mus musculu
36	117	17.2	503	4	P97797	p97797 mus musculu
37	116	17.1	418	11	P78324	p78324 rattus norv
38	115.5	17.0	513	11	Q99KA4	Q99ka4 homo sapien
39	115	16.9	487	11	O70426	o70426 mus musculu
40	115	16.9	509	11	O08907	o08907 mus musculu
41	113.5	16.7	334	13	Q91B05	Q91b05 sphoeroides
42	111	16.4	361	4	Q9H1U5	Q9h1u5 homo sapien
43	110.5	16.2	372	4	Q9Y4V0	Q9y4v0 homo sapien
44	110.5	16.2	473	11	Q9D8L4	Q9d8l4 mus musculu
45	110	16.2	123	11	O61243	o61243 mus musculu

ALIGNMENTS

RESULT 1
Q9UL77

```
ID   Q9UL77      PRELIMINARY;   PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035037; AAD56273.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11738 MW;   C06681716C4D16F3 CRC64;
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Query Match   57.3%;   Score 389.5;   DB 4;   Length 108;
Best Local Similarity   68.2%;   Pred. No. 5.6e-35;
Matches   73;   Conservative 13;   Mismatches 20;   Indels 1;   Gaps 1;

```
Qy  21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
        ||||||||||||||| :| :|||||: | |::|:||||: ||| |||| ||: ||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK 126
        |||| | |:| |:|||:|:| | :||||| |:|||||||||||||||
Db  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK 126
```

```
Db    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
         |||||||| |::|  |||::||||  | |||:|| |||| ||||||
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RESULT 2

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ID   Q9R1A5                  PRELIMINARY;       PRT;    214 AA.
AC   Q9R1A5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab7, its light and heavy chains) and construction of a
RT   single chain antibody (scFv).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF152371; AAD40242.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     214    214
SQ   SEQUENCE   214 AA;  23922 MW;  52BA205FDE995E2A CRC64;

Query Match     Best Local Similarity   56.0%;     Score 380.5;  DB 11;  Length 214;
Matches   72;  Conservative   14;  Mismatches   20;  Indels    1;  Gaps    1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||:|||||||||||:|  ||||| || |:|  | | |:|| ||| | |:::|:||
Db    1 DIQLTQSPSMYASLGERVTITCKASQDINSYLSWFQQKPGKPGKSPKTLIYRANRLVDGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
         |||||||| |::|||:|| |||||||| |||:| :||| ||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYCLQYDEPPTFGSGTKLEIK 107
```

RESULT 3

```
ID   Q9UL70                  PRELIMINARY;       PRT;    108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunopathol. 87:184-192(1999).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;

Query Match     Best Local Similarity   55.7%;     Score 378.5;  DB 4;  Length 108;
Matches   72;  Conservative   16;  Mismatches   18;  Indels    1;  Gaps    1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||||||||||:| :||||| || |:|  | | |:|| ||| | |:::|:||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
         |||||||| |::| |||:|||:||||| ||| |:: ||| |||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107
```

RESULT 4

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ID   Q9JL84                  PRELIMINARY;       PRT;    107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206022; AAF69320.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11648 MW;  ACF9B1253ACA1E5D CRC64;

Query Match     Best Local Similarity   54.8%;     Score 372.5;  DB 11;  Length 107;
Matches   73;  Conservative    7;  Mismatches   26;  Indels    1;  Gaps    1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
         ||||||| ||||||| :|  || || |:|  || | || | |:|| ||| |:: |:||
Db    1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYTSSLXSGVPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
         |||||||| |||:||||||||||||| || :|  |||||||||
Db   61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107
```

RESULT 5

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ID   Q9UL81                  PRELIMINARY;       PRT;    107 AA.
AC   Q9UL81;
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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
FT   NON_TER   107   107
SQ   SEQUENCE   107 AA; 11501 MW; 070549FDE0754748 CRC64;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
               |||||||| |||||:|| |||||| :| ||:|:|:|||||||:||||||:|:|| ||:|||
Db   1 DIQMTQSPFSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy   81 RFSGSGSGGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
               |||||||| ||::| :| | ||:|||||:| ||| || |||||:||:
Db   61 RFSGSGSGTDFLTLISGLQAEDFATYYCQQSYSALTFGPGTKVDIR   106

RESULT 6

ID   Q9UL79   PRELIMINARY;   PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match   53.2%; Score 362; DB 4; Length 107;
Best Local Similarity   64.2%;
  Matches   68; Conservative   15; Pred. No. 5.5e-32; Mismatches   23; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
               |||||||| |||||:|| |||||| :| ||:|:|:|||||||:||||||:|:|| ||:|||
Db   1 DIQMTQSPFSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy   81 RFSGSGSGGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
               |||||||| ||::| :| | ||:|||||:| ||| || |||||:||:
Db   61 RFSGSGSGTDFLTLISGLQAEDFATYYCQQSYSALTFGPGTKVDIR   106

Query Match   51.0%; Score 346.5; DB 4; Length 108;
Best Local Similarity   64.5%;
  Matches   69; Conservative   12; Pred. No. 2.7e-30; Mismatches   25; Indels   1; Gaps   1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
               ||:||||||||||||:|| ||| :||:||:| :|||||||:|||:||||:|:|| ||:|||
Db   1 DIVMTQSPSSLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASSLQSGVPS 60

Qy   81 RFSGSGSGGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
               |||||||| ||:| :|:|:|| |||||||:||: :||||||||:||:|
Db   61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYSFPPTFGGGTKVEIK   107

RESULT 7

ID   Q9QYF0   PRELIMINARY;   PRT;   298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   8 SCFV.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RA   Shinohara N., Demura T., Fukuda H.;
RT   "Isolation of a novel type of vascular cell wall-specific monoclonal
RT   antibody recognizing a cell polarity using a phage display subtraction
RT   method.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match   50.2%; Score 341.5; DB 11; Length 298;
Best Local Similarity   57.7%;
  Matches   64; Conservative   18; Pred. No. 3e-29; Mismatches   28; Indels   1; Gaps   1;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                   |||:||||||||||||:|| |||:|||:|||:| :|:|||| | :|:|::| :
Db   169 GGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQOKGKSPQLLVVNAKTLAD   228

Qy   77 GIPSRFSGSGSGGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
               ||:|||||||||| || :|:|:|| |||:|| ||: :||||||||||||||
Db   229 GVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQOHFWTTPYTFGGGTKLEIK   279

RESULT 8

ID   Q9UL78   PRELIMINARY;   PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035036; AAD56272.1; -.
DR   HSSP; P01789; IMCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    109    109
SQ   SEQUENCE   109 AA;   11646 MW;   5F675C52EC7EE197 CRC64;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDI-NKYMAWYQHKPGKRPRLLIHYTSALQPGIP  79
Db    1  EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP  60

Qy   80  SRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK  126
Db   61  DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK  108
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Query Match       46.9%;   Score 319;   DB 4;   Length 109;
Best Local Similarity   57.4%;   Pred. No. 2.7e-27;
Matches   62;   Conservative   17;   Mismatches   27;   Indels   2;   Gaps   2;
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RESULT  9
Q99M37

ID   Q99M37       PRELIMINARY;   PRT;   238 AA.
AC   Q99M37;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:5947).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY TUMOR;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002035; AAH02035.1; -.
SQ   SEQUENCE   238 AA;   26344 MW;   FB2B06A0B801330A CRC64;
```

```
Query Match       46.7%;   Score 317.5;   DB 11;   Length 238;
Best Local Similarity   47.0%;   Pred. No. 9.6e-27;
Matches   62;   Conservative   26;   Mismatches   37;   Indels   7;   Gaps   3;
```

```
Qy    1  MRPSIQFLGILLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI-----NKYMAW  55
Db    1  MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEW  59

Qy   56  YQHKPGKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-  114
Db   60  YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP  119

Qy  115  WTFGGGTKLEIK  126
Db      ,
```

```
Db  120  YTFGGGTKLEIK  131
```

```
RESULT  10
Q9UL85

ID   Q9UL85       PRELIMINARY;   PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035029; AAD56265.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    109    109
SQ   SEQUENCE   109 AA;   11761 MW;   FB1E43E7C7AFACCC CRC64;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS  80
Db    1  EIVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPA  60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWIW----TFGGGTKLEIK  126
Db   61  RFSGSGSGTEFTLTISSLQSEDFAIVHCQQY-NSWPLTFGGGTKVEIK  108
```

```
Query Match       45.6%;   Score 310;   DB 4;   Length 109;
Best Local Similarity   56.0%;   Pred. No. 2.6e-26;
Matches   61;   Conservative   18;   Mismatches   26;   Indels   4;   Gaps   2;
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RESULT  11
Q9UL86

ID   Q9UL86       PRELIMINARY;   PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035028; AAD56264.1; -.
DR   HSSP; P01789; IMCP.
```

```
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;

Query Match            45.3%;  Score 308;  DB 4;  Length 109;
Best Local Similarity  54.6%;  Pred. No. 4.3e-26;
Matches  59;  Conservative  20;  Mismatches  27;  Indels   2;  Gaps   2;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDI-NKYMAWYQHKPGKRPRLLIHYTSALQPGIP 79
          : ::||| ||||||| ||||| |:: || ||| :|||||| | ||||||| ||: ||||
Db    1  EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

Qy   80  SRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
          |||||  || |||| |||||:||  |||||||  :|||:|||||||||
Db   61  DRFSGSGSEETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108
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RESULT 12
ID   Q9UL83      PRELIMINARY;        PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035031; AAD56267.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;

Query Match            44.98%;  Score 305.5;  DB 4;  Length 108;
Best Local Similarity  53.7%;   Pred. No. 8e-26;
Matches  58;  Conservative  21;  Mismatches  26;  Indels   3;  Gaps   2;

Qy   21  DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPSRFS 80
Db    1  EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60

Qy   81  RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
Db   61  RFSGSGSGTEFTLTISSLQPEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107
```

```
RESULT 13
ID   Q9U410      PRELIMINARY;        PRT;   106 AA.
AC   Q9U410;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC   Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC   Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the light chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF207620; AAF19434.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     106     106
SQ   SEQUENCE   106 AA;  11478 MW;  F20F544426BAE63E CRC64;

Query Match            44.08%;  Score 299;  DB 5;  Length 106;
Best Local Similarity  57.7%;   Pred. No. 4e-25;
Matches  60;  Conservative  14;  Mismatches  28;  Indels   2;  Gaps   2;

Qy   24  MTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPSRFS 83
Db    4  LTQSPAIMSASPGEKVTMTCSASSSVS-YVYWYLQKPGSSPRLLIYDTSNLASGVPVRFS 62

Qy   84  GSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
Db   63  GSGSGTSYSLTISRMEAEDAATYYCQQWTSYPFTFGSGTKLEIK 106
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RESULT 14
ID   Q9ER29      PRELIMINARY;        PRT;   107 AA.
AC   Q9ER29;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT   "Cloning and sequencing of the light chain fragment of variable region
RT   genes of an anti-hTNF-a monoclonal antibody.";
RL   J. Cell. Mol. Immunol. 12:21-26(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT   "Construction and sequencing of the single-chain antibody gene of a
RT   human TNF-alpha specific monoclonal antibody.";
RL   Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF262753; AAG23804.1; -.
```

```
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      107    107
SQ   SEQUENCE   107 AA;  11784 MW;  2B15EEA6604A26C3 CRC64;

Query Match             43.5%;  Score 295.5;  DB 11;  Length 107;
Best Local Similarity   51.4%;  Pred. No. 9.7e-25;
Matches   55;  Conservative   21;  Mismatches   24;  Indels    7;  Gaps     2;

Qy    24  MTQSPSSLSASLGGKVTITCKTSQDI------NKYMAWYQHKPGKRPRLLIHYTSALQPG  77
          ||||||||| |:| ||||: ||||||      ||||||||::|:|||||||:::| ||||
Db     1  MTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAWYQKKPGQSPELLVFASTRESG  60

Qy    78  IPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKL  123
          :|:|| |||||| |::: ||:|| ||:|:||| |:|||||||||||
Db    61  VPDRFMCGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL  107

RESULT 15
Q9JL78
ID   Q9JL78        PRELIMINARY;      PRT;   101 AA.
AC   Q9JL78;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A.CA;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206028; AAF69326.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER        1      1
FT   NON_TER      101    101
SQ   SEQUENCE   101 AA;  10778 MW;  0A7F65E6A7E6F14D CRC64;

Query Match             43.0%;  Score 292.5;  DB 11;  Length 101;
Best Local Similarity   56.4%;  Pred. No. 1.9e-24;
Matches   57;  Conservative   16;  Mismatches   25;  Indels    3;  Gaps     2;

Qy    29  SSLSASLGGKVTITCKTSQDI-NKYMAWYQHKPGKRPRLLIHYTSALQPGIPSRFSGSGSGS  87
          :::||| | |:||||| ||| |||| ||:|||| |:||||:::|||||:|::|||||||||||
Db     1  TTMAASPGEKITITCSASSISSNYLHWYQQKPGFSPKLLIYRTSNLASGVPTRFSGSGSGS  60

Qy    88  GRDYSFNISNLEPEDIATYYCLQYDNL--WTFGGGTKLEIK  126
          | ||:||:||||:| |::  ||| :  :||||||||||||
Db    61  GTSYSLTIGTMEAEDVATYYCQQGSSIPRYTFGGGTKLEIK  101

Search completed: May  7, 2002, 12:31:42
Job time: 638 sec
```

OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: May 7, 2002, 12:22:24 ; Search time 67.39 Seconds
(without alignments)
153.884 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVFLMAVVTGVNSE..........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : A_Geneseq_1101:*
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 9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	746	100.0	140	16	AAR81327	Mouse VLA-4 antibo
2	746	100.0	140	16	AAW22410	Alpha-4 integrin m
3	645	86.5	123	16	AAR81330	Mouse anti-VLA-4 a
4	633	84.9	136	17	AAW04379	Chimeric human/mu
5	629	84.3	140	12	AAR11384	Variable gamma hea
6	625	83.8	136	16	AAR76664	Murine ONS-21 anti
7	595	79.8	136	14	AAR41679	V heavy chain of r
8	593.5	79.6	137	18	AAR21845	Heavy chain variab
9	591	79.2	138	19	AAW63828	Human Mab #117-10C
10	584	78.3	142	16	AAR81333	Human VLA-4 reshap
11	584	78.3	142	18	AAW22428	Humanised alpha-4
12	576.5	77.3	135	21	AAB07967	Amino acid sequenc
13	570.5	76.5	137	17	AAR95948	HNK-20 variable he
14	544	72.9	123	16	AAR81323	Humanized VLA-4 an
15	539.5	72.3	135	21	AAB07969	A heavy chain vari
16	537	72.0	123	18	AAW22413	Humanised alpha-4
17	535.5	71.8	437	19	AAW37738	Nucleotide sequenc
18	524.5	70.3	122	21	AAY53590	Heavy chain from a
19	521.5	69.9	122	14	AAR30767	Heavy chain variab
20	521.5	69.9	120	19	AAR44121	Heavy chain variab
21	518.5	69.5	113	15	AAR60527	Heavy chain variab
22	517	69.3	143	15	AAR59942	Anti-VLA4 rAb huma
23	516.5	69.2	120	16	AAR79889	Anti-EGFR antibody
24	516	69.2	121	20	AAW96741	Heavy chain variab
25	513	68.8	121	14	AAR39817	Heavy chain variab
26	511	68.5	120	15	AAR38749	HP1/2 Vh. Homo sa
27	511	68.5	120	20	AAY23984	Anti-VLA4 Ab HP1/2
28	511	68.5	120	20	AAY01033	Antibody HP1/2 hea
29	511	68.5	120	22	AAB73462	Anti VLA-4 antibod
30	509.5	68.3	126	20	AAR15439	Murine anti-VLA-4
31	509	68.3	120	22	AAR39566	Heavy chain variab
32	508	68.1	120	14	AAY56873	Sequence of the va
33	505.5	67.8	138	21	AAW29750	MAb CT-M-01 heavy
34	505.5	67.8	139	18	AAY30117	Anti-HMFG MAb CTMO
35	504	67.6	254	20	AAY30119	Murine anti-botuli
36	504	67.6	254	20	AAY30121	Murine anti-botuli
37	504	67.6	254	20	AAY30121	Murine anti-botuli
38	504	67.6	254	20	AAB82701	Murine anti-botuli
39	503	67.4	136	22	AAR76681	Murine anti-botuli
40	502	67.3	136	16	AAR04396	Human/murine chime
41	502	67.3	136	17	AAW04396	Human/murine chime
42	501.5	67.2	116	12	AAR15437	Chimeric human/mu
43	501.5	67.2	240	12	AAR15443	VEGF antagonist an
44	501	67.2	119	19	AAW63820	VEGF antagonist an
45	501	67.2	248	19	AAW63830	Human Mab #117-10C

ALIGNMENTS

```
RESULT   1
AAR81327

ID   AAR81327 standard; Protein; 140 AA.
XX
AC   AAR81327;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
DE   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key          Location/Qualifiers
FH
FT   Peptide      1..19
FT                /note= "signal peptide"
FT   Region       20..49
FT                /note= "framework region 1"
FT   Region       50..54
FT                /note= "complementarity determining region 1"
FT   Region       55..68
FT                /note= "framework region 2"
FT   Region       69..85
FT                /note= "complementarity determining region 2"
FT   Region       86..117
FT                /note= "framework region 3"
FT   Region       118..131
FT                /note= "complementarity determining region 3"
FT   Region       132..140
FT                /note= "framework region 4"
XX
PN   WO9519790-A1.
```

XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-0186269.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99892.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 2; 105pp; English.
XX

CC   The sequence represents the mouse antibody 21.6 heavy chain variable
CC   region directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC   linked to human constant regions in the construction of a humanised
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (see AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanised heavy chain, amino acids H27,
CC   H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig H chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanised antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   140 AA;

Query Match   100.0%; Score 746; DB 16; Length 140;
Best Local Similarity   100.0%; Pred. No. 5.9e-60;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1 MKCSWVMFFLMAVVTGVNSEVQOLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 mkcswvmfflmavvtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrp 60

Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATTIADTSSNTAYLQLSSLTSEDTPAVYFCAREGY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 eqglewigridpangytkydpkfqgkattiadtssntaylqlssltsedtavyfcaregy 120

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
           ||||||||||||||||||||
Db   121 ygnygvyamdywgqgtsvtv 140
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RESULT 2
AAW22410
ID   AAW22410 standard; Protein; 140 AA.
XX
AC   AAW22410;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Alpha-4 integrin mouse Mab 21.6 VH region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
XX
FH   Key   Location/Qualifiers
FT
FT   Peptide   1..19
FT   /label= Leader
FT   Region   20..49
FT   /label= FR1
FT   /note= "framework region 1"
FT   Region   50..54
FT   /label= CDR1
FT   /note= "complementarity determining region 1"
FT   Region   55..68
FT   /label= FR2
FT   /note= "framework region 2"
FT   Region   69..85
FT   /label= CDR2
FT   /note= "complementarity determining region 2"
FT   Region   86..117
FT   /label= FR3
FT   /note= "framework region 3"
FT   Region   118..131
FT   /label= CDR3
FT   /note= "complementarity determining region 3"
FT   Region   132..140
FT   /label= FR4
FT   /note= "framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74760.
XX
PF   21-NOV-1996; 96WO-US18807.
XX
PR   21-NOV-1995; 95US-0561521.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 69-70; 107pp; English.
XX

CC   This polypeptide comprises the heavy chain variable region (VH) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC   complementarity determining regions (CDRs) of the 21.6 VH can be
CC   incorporated into a human 21/28'CL framework to produce a claimed
CC   humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   140 AA;

Query Match   100.0%; Score 746; DB 18; Length 140;
Best Local Similarity   100.0%; Pred. No. 5.9e-60;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 mkcswvmfflmavvtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrp 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 eqglewigridpangytkydpkfqgkatitadtssntaylqlssltsedtavyfcaregy 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
        ||||||||||||||||||||
Db 121 ygnygvyamdywgqgtsvtv 140

RESULT 3
ID   AAR81330 standard; Protein; 123 AA.
XX
AC   AAR81330;
XX
DT   02-APR-1996 (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FH
FT   Region   1..30
FT   /label= FR1
FT   /note= "mouse heavy chain variable framework
FT   region 1"
FT   Region   31..35
FT   /label= CDR1
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 1"
FT   Region   36..49
FT   /label= FR2
FT   /note= "mouse heavy chain variable framework
FT   region 2"
FT   Region   50..66
FT   /label= CDR2
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 2"
FT   Region   67..98
FT   /label= FR3
FT   /note= "mouse heavy chain variable framework
FT   region 3"
FT   Region   99..112
FT   /label= CDR3
FT   /note= "mouse heavy chain variable complementarity
FT   determining region 3"
FT   Region   113..123
FT   /label= FR4
FT   /note= "mouse heavy light chain variable framework
FT   region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX

PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 68; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   123 AA;

Query Match   86.5%; Score 645; DB 16; Length 123;
Best Local Similarity   100.0%; Pred. No. 6.5e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 120

Qy 140 V 140
        |
Db 121 v 121

RESULT 4
ID   AAW04379 standard; Protein; 136 AA.
XX
AC   AAW04379;
XX
DT   04-DEC-1996 (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 variable heavy region.
XX
KW   Heavy; variable region; murine; human; myeloblastoma; chimaera;
KW   monoclonal antibody; chimera; single stranded Fv region;
KW   low human antigenicity; diagnosis; treatment; cerebral tumour;
KW   reshaped.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..19
FT   /label= sig_peptide
FT   Peptide   20..136
FT   /label= mat_peptide
FT   Region   50..54
FT   /label= CDR_1
FT   Region   69..85
FT   /label= CDR_2
FT   Region   118..125
FT   /label= CDR_3

PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994; 94JP-0285057.
XX
PR   18-OCT-1994; 94JP-0252166.
PR   19-NOV-1993; 93JP-0291078.
XX
PA   (CHUS) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38600.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 2; Page 22; 45pp; Japanese.
XX
CC   The present sequence is the variable heavy region of the
CC   chimeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb
CC   was prepd. by combining light and heavy variable region DNA,
CC   from a murine anti-human myeloblastoma cell MAb, with human light
CC   and heavy constant region sequences, respectively to produce
CC   chimeric human/murine light and heavy chain DNA mols.. A
CC   recombinant vector for the expression of the heavy and light chain
CC   DNA mols. was prepd., and used to transform a host cell. The host
CC   cell was then cultured, and the expression prods. of the heavy and
CC   light chain DNA mols. sepd. and connected with a peptide linker to
CC   produce a single stranded Fv region. The reshaped Fv region has
CC   low human antigenicity, and is therefore expected to be useful as
CC   an agent for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   136 AA;

Query Match   84.9%; Score 633; DB 17; Length 136;
Best Local Similarity   89.3%;
Matches 125; Conservative   2; Pred. No. 8.8e-50; Mismatches   7; Indels   6; Gaps   2;

Qy   1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                ||||||||||||||||| |||:|||||||||||||||||||||||||||||||| |||
Db   1 mkcswvmfflmaavtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtyihwakqrp 60

Qy   61 EQGLEWIGRIDPANGYTKDPDKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                |||||||||||||:.|||||| ||||||||||||||||||||||||||||||| ||
Db   61 eqglewigridpadgntkydpkfqgkatitadtssntaylqlssltsedtavyyca-say 119

Qy   121 YGNYGVYAMDIWGQGTSVTV 140
                ||| |:|||||||||||
Db   120 yvn----qdywggtsvtv 134

RESULT 5
ID   AAR11384 standard; Protein; 140 AA.
AC   AAR11384;
DT   08-MAY-1991 (first entry)
DE   Variable gamma heavy chain of T84.66 monoclonal antibody.
KW   MAb T84.66; gamma heavy chain; carcinoembryonic antigen; CEA;
KW   human adenocarcinoma; mouse-human chimaeric antibody.
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT   Peptide   20..38

FT   /label= tryptic peptide
FT   /note= "sequenced as peptide fragment"
FT   Peptide   39..49
FT   /label= tryptic peptide
FT   /note= "sequenced as peptide fragment"
FT   Peptide   55..59
FT   /label= tryptic peptide
FT   /note= "sequenced as peptide fragment"
FT   Region   50..54
FT   /label= complementarity determining region
FT   Region   69..85
FT   /label= complementarity determining region
FT   Region   118..130
FT   /label= complementarity determining region
XX
PN   WO9101990-A.
XX
PD   21-FEB-1991.
XX
PF   19-JUL-1990; 90WO-US04049.
XX
PI   Shively JE, Riggs AD, Neumaier M;
XX
PA   (CITY) CITY OF HOPE.
XX
PR   26-JUL-1989; 89US-0385102.
XX
DR   WPI; 1991-073486/10.
DR   N-PSDB; AAQ11098.
XX
PS   Claim 4; Page 18; 24pp; English.
XX
PT   Novel anti-CEA antibody - comparable to ATCC Accession NO. BH
PT   8747, produced by recombinant DNA, used in diagnosis of tumours
XX
CC   The heavy chain variable region of murine MAb 84.66 was cloned and
CC   sequenced. It was used to produce mouse V-human C antibodies with high
CC   affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to
CC   diagnose human colon adenocarcinomas.
CC   See also AAQ10834-Q10848.
XX
SQ   Sequence   140 AA;

Query Match   84.3%; Score 629; DB 12; Length 140;
Best Local Similarity   87.9%;
Matches 123; Conservative   6; Pred. No. 2.1e-49; Mismatches   9; Indels   2; Gaps   1;

Qy   1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                ||||||:|||||||||||||||||||||||:|||||||||||||||||||||||:| |||
Db   1 mkcswvifflmaavtgvnsevqlqqsgaelvepgasvklsctasgfnikdtyihwvkqrp 60

Qy   61 EQGLEWIGRIDPANGYTKDPDKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                |||||||||||||| |:||||||||||||||||||||||||||||||||||:|| ||
Db   61 eqglewigridpangnskyvpkfqgkatitadtssntaylqlssltsedtavyycapfgy 120

Qy   121 YGNYGVYAMDIWGQGTSVTV 140
                | ||:||||||||||
Db   121 y--vsdyamaywgqgtsvtv 138

RESULT 6
ID   AAR76664 standard; Protein; 136 AA.
AC   AAR76664;
DT   16-JAN-1996 (first entry)
DE   Murine ONS-21 antibody variable heavy chain.
KW   Plasmid pUC-M21-V(H); murine; ONS-M21 antibody; chimeric protein;
KW   medulloblastoma; brain tumour; treatment; diagnosis.

Left column

```
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FH
FT   Peptide        1..19
FT                  /label= sig_peptide
FT   Peptide        20..136
FT                  /label= mat_peptide
XX
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994; 94WO-JP01763.
XX
PR   19-NOV-1993; 93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T, Sato K, Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94485.
XX
PS   Claim 14; Page 59; 120pp; Japanese.
XX
CC   AAQ94485 is the plasmid pUC-M21-V(H), which encodes AAR76664 the
CC   murine antibody ONS-21 variable heavy chain. The plasmid was
CC   used in the construction of an expression vector, contg. cDNA
CC   encoding a human/murine chimeric antibody, reactive with
CC   human medulloblastoma (a brain tumour) cells. The chimeric
CC   antibody can be used in the diagnosis and treatment of this
CC   disease.
XX
XX
SQ   Sequence   136 AA;

  Query Match             83.8%;  Score 625;  DB 16;  Length 136;
  Best Local Similarity   88.6%;  Pred. No. 4.6e-49;
  Matches   124;  Conservative    2;  Mismatches    8;  Indels    6;  Gaps    2;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |||||||||||||||||| ||||||||||||||||||||||||||||||||| |||||
Db    1 mkcswvmfflmavvtgvnsevqlqqsgraelvkpgasvklsctasgfnikdtylhwakqrp 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATTTADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||||:|| |||||||||||||||||||||||||||||||||||||||::||
Db   61 eqglewigridpadgntkydpkfqgkatitadtssntaylqlsslitsedtavyyca-say 119

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
          || | ||||||||||||||
Db  120 yvn----qdywgqgtsvtv 134
```

RESULT 7

AAR41679
```
ID   AAR41679 standard; Protein; 136 AA.
XX
AC   AAR41679;
XX
DT   24-MAR-1994 (first entry)
XX
DE   v heavy chain of recombinant anti-feline calicivirus antibody.
XX
KW   Antibody; feline calicivirus; FCV; neutralise; heavy chain; virus;
KW   infection; diagnosis; treatment; prophylaxis.
XX
OS   Synthetic.
XX
```

Right column

```
FH   Key            Location/Qualifiers
FT   Domain         47..54
FT                  /label= Complementary Determining Region 1.
FT   Domain         69..86
FT                  /label= Complementary Determining Region 2.
FT   Domain         118..125
FT                  /label= Complementary Determining Region 3.
XX
PN   EP561194-A.
XX
PD   22-SEP-1993.
XX
PF   26-FEB-1993; 93EP-0103066.
XX
PR   28-FEB-1992; 92JP-0079189.
XX
PA   (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
XX
PI   Kimachi K, Maeda H, Mikami T, Nishiyama K, Tohya Y;
PI   Tokiyoshi S;
XX
DR   WPI; 1993-296521/38.
DR   N-PSDB; AAQ48001.
XX
PS   Claim 1-2; Figure 3; 36pp; English.
XX
CC   Anti-feline calicivirus recombinant antibody - used to treat,
CC   prevent and diagnosis infection and is safe but effective in cats
XX
XX
CC   The gene fragment encoding the v heavy chain region is used to
CC   produce a genetically engineered antibody capable of reacting
CC   specifically with feline calicivirus (FCV). The antibody can be used
CC   to treat, prevent and diagnose FCV infection. It has a broad virus-
CC   neutralising spectrum and can be used to neutralise viruses which
CC   have acquired immunity to other neutralising antibodies.
XX
SQ   Sequence   136 AA;

  Query Match             79.8%;  Score 595;  DB 14;  Length 136;
  Best Local Similarity   82.9%;  Pred. No. 2.3e-46;
  Matches   116;  Conservative    8;  Mismatches   10;  Indels    6;  Gaps    1;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||||| :||||||||||||||||||||||||||||||||||||||||||| :||:|||
Db    1 mkcswvifflmavvtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtynhwvkqrp 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATTTADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          |||||||||||||||| |||||:|||||:|||||||||||||::||:|||||||:||
Db   61 eqglewigridpangnthaylqvnsltsedtavyycasggn 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
          :  |||||| |||
Db  121 aw-----laywgggtlvtv 134
```

RESULT 8

AAW21845
```
ID   AAW21845 standard; Protein; 137 AA.
XX
AC   AAW21845;
XX
DT   19-DEC-1997 (first entry)
XX
DE   Heavy chain variable region of KM1486 antibody.
XX
KW   Complementarity determining region; CDR; heavy chain; treatment;
KW   variable region; murine; mouse; human; interleukin 5; IL-5;
KW   receptor; alpha chain; monoclonal antibody; hybridoma; detection;
KW   assay; diagnosis; allergic respiratory disease;
KW   chronic bronchitis.
XX
OS   Mus spp.
```

```
FH   Key              Location/Qualifiers
FT   Peptide          1..19
FT                    /label= sig_peptide
FT   Peptide          20..137
FT                    /label= mat_peptide
FT   Region           50..54
FT                    /label= mat_peptide
FT   Region           69..85
FT                    /label= complementarity_determining_region_1
FT   Region           118..126
FT                    /label= complementarity_determining_region_2
FT                    /label= complementarity_determining_region_3
XX
DR   WPI; 1997-202249/18.
DR   N-PSDB; AAY73612.
XX
PN   WO9710354-A1.
XX
PD   20-MAR-1997.
XX
PF   11-SEP-1996;   96WO-JP02588.
XX
PR   11-SEP-1995;   95JP-0232384.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Anazawa H,  Furuya A,  Hanai N,  Iida A,  Koike M;
PI   Nakamura K,  Takatsu K;
XX
PT   Antibody against alpha-chain of human interleukin 5 receptor -
PT   useful for diagnosis and treatment of respiratory allergic diseases,
PT   e.g. chronic bronchitis
XX
PS   Example 2; Pages 124-125; 238pp; Japanese.
XX
CC   The present sequence is the heavy chain variable region of the
CC   murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha)
CC   monoclonal antibody (MAb) KM1486. KM1486 is produced by the hybridoma
CC   FERM BP-5651, which was prepared by immunising Balb/c mice with
CC   hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
CC   myeloma P3-U1 cells and screening the resultant hybridomas. The MAb
CC   can be used to detect or assay for hIL-5R alpha and cells
CC   expressing it on their surface, especially to diagnose allergic
CC   respiratory diseases, e.g. chronic bronchitis. It can also be used
CC   to treat such diseases.
XX
SQ   Sequence 137 AA;

Query Match             79.6%;  Score 593.5;  DB 18;  Length 137;
Best Local Similarity   82.9%;  Pred. No. 3.2e-46;
Matches 116;  Conservative 6;  Mismatches 13;  Indels 5;  Gaps 1;

Qy    1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
         |||||||||||||||||||||||||||||||||||||||||||||::|||::||||
Db    1  mkcswviffimavvtgvnsevqlqqsgaelvkpgasvnlsctasgfnikdtymhwvkqrp  60

Qy   61  EQGLEWIGRIDPANGYTKYDPKFQGKATIPADTSSNTAYLQLSSLTSEDTAVFCAREGY  120
         ||||||||||||| ||:||||||| |:|||||||||||||||||||||||||||||:|
Db   61  eqglewigridpangntksdpkfqgakatiaadtssntaylqlssltsedtavyyct---  116

Qy  121  YGNYGVYAMDYWGQGTSVTIV  140
         |||||||:||:||
Db  117  -gglrlrfdywgqgttltv  135
```

```
RESULT   9

ID   AAW63828 standard; Protein; 138 AA.
XX
AC   AAW63828;
XX
DT   28-SEP-1998 (first entry)
```

```
XX
DE   Human Mab #117-10C heavy chain variable region protein fragment.
XX
KW   Interleukin-18; IL-18; human; treatment; autoimmune disease; Mab;
KW   immunosuppressant; inhibitor; receptor protein; detection; heavy chain;
KW   monoclonal antibody; Mab; variable region.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   Peptide          1..19
FT                    /label= signal
FT   Protein          20..138
FT                    /label= Mab 117-10C heavy chain variable region
XX
PN   EP850952-A1.
XX
PD   01-JUL-1998.
XX
PF   23-DEC-1997;   97EP-0310555.
XX
PR   28-JUL-1997;   97JP-0215490.
PR   26-DEC-1996;   96JP-0356426.
PR   21-FEB-1997;   97JP-0052526.
PR   06-JUN-1997;   97JP-0163490.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI   Kunikata T,  Kurimoto M,  Torigoe K,  Ushio S;
XX
DR   WPI; 1998-335317/30.
DR   N-PSDB; AAV44000.
XX
PT   New interleukin-18 receptor protein used to inhibit interleukin-18,
PT   to treat autoimmune disease and as immunosuppressant - and new
PT   monoclonal antibody and hybridoma used to detect interleukin-18
PT   receptor protein
XX
PS   Example 3.3a; Page 22; 35pp; English.
XX
CC   This sequence represents the human monoclonal antibody (Mab) #117-10C
CC   heavy chain variable region which is used in a method involved in
CC   neutralising IL-18 or to treat autoimmune diseases or as an
CC   immunosuppressant using anti-IL-18 antibodies which can inhibit IL-18.
CC   Such antibodies can also be used to detect the IL-18 receptor protein
CC   (labelled with an enzyme or a radioactive or fluorescent substance). The
CC   protein is used to treat e.g. graft rejection, pernicious anaemia,
CC   atrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis,
CC   discoid lupus erythematosis, ulcerative colitis, cold-agglutinin-relating
CC   diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic
CC   ophthalmitis, hyperthyroidism, Juvenile onset type diabetes, Sjogren
CC   syndrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia
CC   gravis, systemic scleroderma, systemic lupus erythematosus, polyleptic
CC   cold haemoglobinuria, polymyositis, periarteritis nodosa, multiple
CC   sclerosis, Addison's disease, purpura haemorrhagica, Basedow's disease,
CC   leukopaenia, Behcet's disease, climacterium praecox, rheumatoid
CC   arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV,
CC   asthma, atopic dermatitis, allergic nasitis, pollinosis,
CC   apitoxin-allergy and septic shock resulting from production or
CC   administration of excessive gamma interferon (IFN-gamma).
XX
SQ   Sequence 138 AA;

Query Match             79.2%;  Score 591;  DB 19;  Length 138;
Best Local Similarity   83.0%;  Pred. No. 5.5e-46;
Matches 117;  Conservative 4;  Mismatches 14;  Indels 6;  Gaps 2;

Qy    1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
         |||||| ||||||||||||||||||||||||||||||||||||||:||::||||
Db    1  mkcswvvflfimavvtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtylywvkqrp  60

Qy   61  EQGLEWIGRIDPANGYTKYDPKFQGKATIPADTSSNTAYLQLSSLTSEDTAVFCAREGY  120
```

```
Db
Qy    61 egglewvgridpangdtkygpnfqdkatitadtssntaylqirslrsedtavyycarrgn 120
            |||| ::||||||| || || || |||||||||||||||||:|||
Qy   121 YG-NYGVYAMDYWGQGTSVTV 140
            || :|| ||||||| |||
Db   121 ygagfg----ywgqgtlvtv 136
```

RESULT 10
AAR81333
ID   AAR81333 standard; Protein; 142 AA.
XX
AC   AAR81333;
XX
DT   23-MAR-1996 (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..19
FT   /note= "signal peptide"
FT   Region   20..49
FT   /note= "framework region 1"
FT   Region   50..54
FT   /note= "complementarity determining region 1"
FT   Region   55..68
FT   /note= "framework region 2"
FT   Region   69..85
FT   /note= "complementarity determining region 2"
FT   Region   86..117
FT   /note= "framework region 3"
FT   Region   118..131
FT   /note= "complementarity determining region 3"
FT   Region   132..142
FT   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99894.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 11; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 heavy
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC   subcloned into mammalian cell expression vectors containing human
CC   kappa or gamma-1 constant regions. In the humanized heavy chain,
CC   amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig H chain. Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells. The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence   142 AA;
```

```
Query Match    78.3%;  Score 584;  DB 16;  Length 142;
Best Local Similarity  77.1%;  Pred. No. 2.4e-45;
Matches 108;  Conservative 15;  Mismatches 17;  Indels 0;  Gaps 0;

Qy     1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
            | :||| ||:|  |:|:|||||||:|||| |:|||||:||||||:||| ||:|:::| :|
Db     1 mdwtwrvfcllavapgahsqvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqap  60
Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            | |:|||||||||||||||:||||||||||||||||||||||:|||||:||||| ||:||
Db    61 gqrlewmgridpangytkydpkfqgrvtitadtsastaymelssirsedtavyycaregy 120
Qy   121 YGNYGVYAMDYWGQGTSVTV 140
            ||||||||||||||||| |||
Db   121 ygnygvyamdywgqgtlvtv 140
```

RESULT 11
AAW22428
ID   AAW22428 standard; Protein; 142 AA.
XX
AC   AAW22428;
XX
DT   09-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..19
FT   /label= Leader
FT   Protein   20..142
FT   /label= Mat_protein
FT   /note= "VH version Ha (Claim 25)"
FT   Region   20..49
FT   /label= FR1
FT   /note= "21/28'CL framework region 1"
FT   Region   50..55
FT   /label= CDR1
FT   /note= "21.6 complementarity determining region 1"
FT   Region   55..67
FT   /label= FR2
FT   /note= "21/28'CL framework region 2"
FT   Region   68..85
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   Region   86..117
FT   /label= FR3
FT   /note= "21/28'CL framework region 3"
FT   Region   118..131
FT   /label= CDR3
FT   /note= "21.6 complementarity determining region 3"
```

FT   Region          132..142
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996; 96WO-US18807.
XX
PR   21-NOV-1995; 95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74789.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 11; 107pp; English.

CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22413). It is composed of complementarity determining regions from
CC   the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human 21/28'CL framework. It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences. The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence 142 AA;

Query Match            78.3%;  Score 584;  DB 18;  Length 142;
Best Local Similarity  77.1%;
Matches  108;  Conservative  15;  Mismatches  17;  Indels  0;  Gaps  0;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          | :| :||:||  ||||||||||||| ||||||||||:||||||||||||||  :|
Db    1 mdwtwrvfclavapgahsqvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqap 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||||||||||:||||||||||:| |||:|||||||||||| ||||||
Db   61 gqrlewmgridpangytkydpkfqgrvtitadtsastaymelssltsedtavycaregy 120

Qy  121 YGNYGYYAMDYWGQGTSVTV 140
         ||||||||||||| || |||
Db  121 ygnygvyamdywggqtltv 140

---

KW   systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW   arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW   multiple sclerosis; transplant rejection; proliferative disease;
KW   leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW   aplastic anaemia; myeloid dysplasia syndrome.
XX
OS   Mus sp.
XX
FH   Key                 Location/Qualifiers
FH
FT   Peptide             1..19
FT                       /note= "signal peptide"
FT   Protein             20..135
FT                       /note= "mature protein"
FT   Region              50..54
FT                       /note= "complementarity determining region 1"
FT   Region              69..85
FT                       /note= "complementarity determining region 1"
FT   Region              118..124
FT                       /note= "complementarity determining region 1"
XX
PN   WO200047625-A2.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US03303.
XX
PR   12-FEB-1999; 99US-0249011.
PR   24-JUN-1999; 99US-0339596.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI   Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR   WPI; 2000-524532/47.
DR   N-PSDB; AAA59696.
XX
PT   Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT   from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT   modulates immune responses and can therefore treat e.g. autoimmune
PT   diseases, infectious diseases -
XX
PS   Example 8; Fig 6A; 162pp; English.

CC   The present sequence represents the heavy chain variable region of the
CC   murine antibody 1F1. The antibody has a binding specificity to B7
CC   molecules. The antibody is used to construct humanized immunoglobulins,
CC   which comprise an antigen binding region of non-human origin and a
CC   portion of a human immunoglobulin. The humanized immunoglobulins are
CC   useful for treating autoimmune diseases, infectious diseases,
CC   inflammatory disorders, systemic lupus erythematosus, diabetes
CC   mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC   inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC   also useful for treating a transplant recipient or preventing transplant
CC   rejection in a transplant recipient, and treating proliferative disease
CC   (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC   thalassemia and aplastic anaemia), inborn errors of metabolism,
CC   congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ   Sequence 135 AA;

Query Match            77.3%;  Score 576.5;  DB 21;  Length 135;
Best Local Similarity  80.7%;
Matches  113;  Conservative  6;  Mismatches  14;  Indels  7;  Gaps  1;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         ||||||:||:||||||||||||:||||||||:|||:|||||:  ||||||||| :|||||
Db    1 mkcswviffimavvtgvnsevhlqqsgaelvrpgalvklsckpsgfnikdtyymhwvkqrp 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         | |||||| |||   | |||||||||| ||||||||||||||||||||||||| |||||
Db   61 egglewigwidpengntlydpkfqgkasitadtssntaylqlssltsedtavyycaregl 120

---

RESULT 12
AAB07967
ID   AAB07967 standard; Protein; 135 AA.
XX
AC   AAB07967;
XX
DT   14-NOV-2000 (first entry)
XX
DE   Amino acid sequence of heavy chain variable region of 1F1 antibody.
XX
KW   Antibody 1F1; B7 molecule; B7; humanised immunoglobulin;
KW   autoimmune disease; infectious disease; inflammatory disorder;

Qy  121 YGNYGYYAMDYWGQGTSVTV 140
         ||||||||||||||||| |||
Db  121 ygnygvyamdywggqtltv 140

RESULT 13

```
Qy   121 YGNYGVYYAMDYWGQGTSVTV 140
         |||||| |||||||| |||
Db   121 f-------faywggtpvtv 133
```

```
AAR95948
ID   AAR95948 standard; Protein; 137 AA.
XX
AC   AAR95948;
XX
DT   10-FEB-1997  (first entry)
XX
DE   HNK-20 variable heavy chain.
XX
KW   Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse;
KW   F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
KW   chimeric antibody; isotype-switched antibody; therapy; infection; human;
KW   pneumonia; bronchiolitis; animal.
XX
OS   Mus musculus.
XX
XX
PN   WO9616974-A1.
XX
PD   06-JUN-1996.
XX
PF   01-DEC-1995;  95WO-US15716.
XX
PR   01-DEC-1994;  94US-0348548.
XX
PA   (ORAV-) ORAVAX INC.
XX
PI   Berdoz J, Kraehenbuhl J;
XX
DR   WPI; 1996-286826/29.
DR   N-PSDB; AAT30458.
XX
PT   DNA encoding variable region of antibody HNK-20 - for treating
PT   respiratory syncytial virus infection
XX
PS   Claim 15; Fig 5d; 75pp; English.
XX
CC   AAR95946-R95948 represent sequences for variable regions of an antibody
CC   produced by the hybridoma cell line HNK-20. This sequence represents
CC   the sequence for the antibody HNK-20 variable heavy chain. HNK-20 is a
CC   murine hybridoma cell line, that produces IgA specific for the F
CC   glycoprotein of respiratory syncytial virus (RSV). The DNA encoding
CC   these sequences were isolated using primers specific for the 5'
CC   untranslated region of the variable region, and for the intron
CC   downstream of the rearranged J region (see AAT30459-T30545 for primer
CC   sequences). The DNA encoding these sequences can be inserted into vectors
CC   containing heterologous (such as human) constant region genes, for the
CC   production of chimeric and isotype-switched antibodies. The antibodies
CC   are useful in the treatment and diagnosis of infection by RSV, such as
CC   pneumonia and bronchiolitis, in humans and animals. By using genomic DNA
CC   as a template, variable region genes can be isolated without producing
CC   fragments that have to be adapted for recombinant antibody expression.
CC   Also, by using the genomic DNA, no knowledge of the DNA sequence
CC   encoding the target variable region is required. Chimeric antibodies
CC   produced from these proteins, that contain the constant region of the
CC   host being treated, are less likely to cause adverse immune reactions.
XX
SQ   Sequence  137 AA;
```

```
Query Match             76.5%;  Score 570.5;  DB 17;  Length 137;
Best Local Similarity   81.4%;  Pred. No. 3.8e-44;
Matches  114;  Conservative    6;  Mismatches   15;  Indels    5;  Gaps    2;

Qy    1 MKCSWVFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        |||||||||||||||||||||||||||||||||| |||||||||||||||| || |||||
Db    1 mkcswvifflmavvtgvnsevqlqqsgaelvrpgalvklsckasgfnikdymywwkqrp 60
```

RESULT 14

```
Qy    61 EQGLEWIGRIDPANGYTKYDPKFQGKAITTADYSSNTAYLQLSSLTISEDTAVFYCAREGY 120
         |||||| ||| |||||| | ||||||||||||:|||||||||||||||||||||||: ||
Db    61 eqglewigwidpengntvydpkfqgkasltadtssntaylqlsslasedtavyyca---y 117
```

```
Qy   121 YGNYGVYYAMDYWGQGTSVTV 140
         |||||| |||||||| |||
Db   118 ygt--syw£pywgggtlvtv 135
```

```
AAR81323
ID   AAR81323 standard; Protein; 123 AA.
XX
AC   AAR81323;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 11; Page 69; 105pp; English.
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   21.6 L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence  123 AA;
```

```
Query Match             72.9%;  Score 544;  DB 16;  Length 123;
Best Local Similarity   82.6%;  Pred. No. 8.2e-42;
Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         :||| |||||  ||||||||||||||||||||||:|:| |  |||||||||||||||||||
Db    1 mkcswviffflmavvtgvnsevqlqqsgaelvrpgalvklsckasgfnikdymywwxqrp 60
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Db   1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrplewmgridpangytky 60
Qy   80 DPKFQGKATITADTSSNTAYIQLSSLTSEDTAVYFCAREGYGNYGVYAMDYWGQGTSVT 139
        ||||:|||||||:::::||||||:::|||||||||||||||||||||||||||||| ||
Qy   80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregygnygvyamdywgqgtlvt 120
Qy 140 v 140
Db 121 v 121

RESULT 15
ID   AAB07969   standard; Protein; 135 AA.
XX
AC   AAB07969;
XX
DT   14-NOV-2000 (first entry)
XX
DE   A heavy chain variable region of humanised 1F1 antibody.
XX
KW   Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW   autoimmune disease; infectious disease; inflammatory disorder;
KW   systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW   arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW   multiple sclerosis; transplant rejection; proliferative disease;
KW   leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW   aplastic anaemia; myeloid dysplasia syndrome.
XX
OS   Synthetic.
OS   Mus sp.
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..19
FT   /note= "signal peptide"
FT   Protein   20..135
FT   /note= "mature protein"
FT   Region   50..54
FT   /note= "complementarity determining region 1"
FT   Region   69..85
FT   /note= "complementarity determining region 1"
FT   Region   118..124
FT   /note= "complementarity determining region 1"
XX
PN   WO200047625-A2.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US03303.
XX
PR   12-FEB-1999; 99US-0249011.
PR   24-JUN-1999; 99US-0339596.
XX
PA   (GEMY) GENETICS INST INC.
XX
PI   Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI   Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR   WPI; 2000-524532/47.
DR   N-PSDB; AAA59698.
XX
PT   Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT   from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT   modulates immune responses and can therefore treat e.g. autoimmune
PT   diseases, infectious diseases -
XX
PS   Example 10; Fig 7A; 162pp; English.
XX
CC   The present sequence represents the heavy chain variable region of the
CC   humanised murine antibody 1F1. The antibody has a binding specificity to
CC   B7 molecules. The antibody is used to construct humanized
CC   immunoglobulins, which comprise an antigen binding region of non-human

CC   origin and a portion of a human immunoglobulin. The humanised
CC   immunoglobulins are useful for treating autoimmune diseases, infectious
CC   diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC   mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC   inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC   also useful for treating a transplant recipient or preventing transplant
CC   rejection in a transplant recipient, and treating proliferative disease
CC   (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC   thalassemia and aplastic anaemia), inborn errors of metabolism,
CC   congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ   Sequence   135 AA;

Query Match   72.3%;   Score 539.5; DB 21; Length 135;
Best Local Similarity   75.0%;   Pred. No. 2.3e-41;
Matches 105; Conservative 11; Mismatches 17; Indels 7; Gaps 1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         ||||||:||||||||||:||||||||:|:|||||||||||||:||:|||:|:|:|:||
Db   1 mkcswviflmavvtgvnsevqlvqsgaevkkpgasvkvsckpsgfnikdyymhwvrqap 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTTSEDTAVYFCAREGY 120
         |||||| ||| ||||||||||||||||:|:||:||||||||||||:|||:||||||| |
Db   61 gqglewigwidpengntlydpkfqgkatitadtstastaymelsslrsedtavyycaregl 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
         |||||| |||
Db 121 f------faywgqgtlvtv 133

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Job time: 246 sec

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                          GenCore version 4.5
                          Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Post-processing: Minimum Match 0%

Run on:        May  7, 2002, 12:23:03 ; Search time 32.41 Seconds
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Title:         US-09-155-739-4
Perfect score: 746
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Total number of hits satisfying chosen parameters:     212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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               2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
               3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
               4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
               5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	Match	DB	ID	Description
1	746	100.0	140	140	5	2	US-08-561-521-4	Sequence 4, Appli
2	746	100.0	140	140	5	2	PCT-US95-01219-4	Sequence 4, Appli
3	645	86.5	123	123	5	2	US-08-561-521-9	Sequence 9, Appli
4	645	86.5	123	123	5	2	PCT-US95-01219-9	Sequence 9, Appli
5	633	84.9	136	136	4	4	PCT-US95-0265A-29	Sequence 29, Appli
6	595	79.8	136	136	1	3	US-08-024-253-2	Sequence 2, Appli
7	593.5	79.6	137	137	5	2	US-08-836-561-31	Sequence 31, Appli
8	584	78.3	142	142	2	5	US-08-561-521-17	Sequence 17, Appl
9	584	78.3	142	142	5	2	PCT-US95-01219-17	Sequence 17, Appl
10	562	75.3	125	125	5	2	US-08-561-521-44	Sequence 44, Appl
11	562	75.3	125	125	5	2	PCT-US95-01219-44	Sequence 44, Appli
12	554	74.1	136	136	4	5	US-08-348-548-8	Sequence 8, Appl
13	554	74.3	136	136	5	2	PCT-US95-15716-8	Sequence 8, Appl
14	544	72.9	123	123	2	2	US-08-561-521-11	Sequence 11, Appl
15	544	72.9	123	123	5	2	PCT-US95-01219-11	Sequence 11, Appl
16	528.5	70.8	120	120	5	5	US-07-934-373C-6	Sequence 6, Appl
17	528.5	70.8	120	120	3	6	US-08-437-642B-6	Sequence 6, Appl
18	528.5	70.8	120	120	5	6	PCT-US93-0782-6	Sequence 6, Appli
19	516	69.2	121	121	2	2	US-08-822-830B-2	Sequence 2, Appli
20	513	68.8	121	121	2	13	US-08-822-830B-13	Sequence 13, Appli
21	511	68.5	120	120	5	2	US-08-950-660-2	Sequence 2, Appl
22	511	68.5	120	120	5	2	PCT-US95-00030-2	Sequence 2, Appl
23	511	68.5	120	120	5	2	PCT-US93-00924-2	Sequence 2, Appli
24	505.5	67.8	138	138	1	5	US-08-603-024-2	Sequence 8, Appli
25	505.5	67.8	139	139	2	5	US-08-253-87C-8	Sequence 8, Appli
26	505.5	67.8	139	139	2	8	US-08-452-164A-8	Sequence 8, Appli
27	504	67.6	254	254	2	4	US-08-792-824-4	Sequence 4, Appli
28	504	67.6	254	254	2	7	US-08-792-824-7	Sequence 7, Appli
29	504	67.6	254	254	2	10	US-08-792-824-10	Sequence 10, Appl
30	504	67.6	254	254	2	13	US-08-792-824-13	Sequence 13, Appl
31	502	67.3	136	136	4	99	US-08-646-265A-99	Sequence 99, Appl
32	500.5	67.1	118	118	2	38	US-08-232-081B-38	Sequence 38, Appl
33	498.5	66.8	113	113	1	2	US-08-207-169A-2	Sequence 2, Appli
34	494.5	66.3	118	118	3	22	US-08-767-128-22	Sequence 22, Appl
35	488.5	65.5	255	255	4	19	US-09-171-945-19	Sequence 19, Appl
36	483.5	64.8	139	139	2	10	US-08-182-067-10	Sequence 10, Appl
37	483.5	64.8	139	139	2	10	US-08-039-198B-10	Sequence 10, Appl
38	482.5	64.7	139	139	2	10	US-08-465-313-10	Sequence 10, Appl
39	475.5	63.7	137	137	1	86	US-08-477-877B-86	Sequence 86, Appl
40	475.5	63.7	137	137	2	86	US-08-472-281A-86	Sequence 86, Appl
41	475.5	63.7	136	136	2	86	US-08-477-989B-86	Sequence 86, Appl
42	475	63.7	117	117	2	18	US-08-290-592E-18	Sequence 18, Appl
43	475	63.7	117	117	5	15	PCT-US95-10053-15	Sequence 15, Appl
44	475	63.7	117	117	5	18	PCT-US96-09448-18	Sequence 18, Appl
45	473.5	63.5	153	153	4	4	US-09-096-244-4	Sequence 4, Appl

ALIGNMENTS

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RESULT
   1
US-08-561-521-4
Sequence 4, Application US/08561521
; Patent No. 584299
; GENERAL INFORMATION:
;   APPLICANT:
;   APPLICANT:   Leger, Olivier J.
;   APPLICANT:   Bendig, Mary M.
;   APPLICANT:   Saldanha, Jose
;   APPLICANT:   Jones, S. Tarran
;   TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION:  Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES:  45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend Khourie and Crew
;   STREET:  One Market Plaza, Steuart Tower, Suite 2000
;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/561,521
;   FILING DATE:
;   CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/186,269A
;   FILING DATE:  25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Smith, William L.
;   REGISTRATION NUMBER:  30,223
;   REFERENCE/DOCKET NUMBER:  15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-543-9600
;   TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  140 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-561-521-4

Query Match            100.0%;  Score 746;  DB 2;  Length 140;
Best Local Similarity  100.0%;  Pred. No. 1.5e-68;
Matches  140;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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Db      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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Db     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
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RESULT 2
Sequence 4, Application PC/TUS9501219
PCT-US95-01219-4

; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-4

Query Match   100.0%; Score 746; DB 5; Length 140;
Best Local Similarity   100.0%; Pred. No. 1.5e-68;
Matches 140; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
          ||||||||||||||||||||
Db    121 YGNYGVYAMDYWGQGTSVTV 140
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Db    121 YGNYGVYAMDYWGQGTSVTV 140
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RESULT 3
US-08-561-521-9
Sequence 9, Application US/08561521
; Patent No. 5840299

; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-9

Query Match   86.5%; Score 645; DB 2; Length 123;
Best Local Similarity   100.0%; Pred. No. 2.2e-58;
Matches 121; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db      1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy     80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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Db     61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy    140 V 140
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Db    121 V 121
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RESULT 4
PCT-US95-01219-9
Sequence 9, Application PC/TUS9501219
; GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US95-01219-9

Query Match   86.5%; Score 645; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.2e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
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Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  60

Qy  80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy 140 V 140
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Db 121 V 121
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RESULT 5
US-08-646-265A-29
Sequence 29, Application US/0864265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-29

Query Match   84.9%; Score 633; DB 4; Length 136;
Best Local Similarity   89.3%; Pred. No. 4.1e-57;
Matches 125; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

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Db   1 MKCSWMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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Db  61 EQGLEWIGRIDPADGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV-SAY 119

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
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Db 120 YVN-----QDYWGQGTSVTV 134
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RESULT 6
US-08-024-253-2
Sequence 2, Application US/0824253
Patent No. 5785968
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: TOHYA, Yukinobu
APPLICANT: MIKAMI, Takeshi
TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

Left column

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COUNTRY: U.S.A.
ZIP: 20036-8218
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC Compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/024,253
  FILING DATE: 19930301
  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 79189/1992
  FILING DATE: 28-FEB-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CANTOR, Herbert I.
  REGISTRATION NUMBER: 24,392
  REFERENCE/DOCKET NUMBER: P-500-23744
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 887-0400
  TELEFAX: (202) 835-0605
  TELEX: 440706 WEGBR
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 136 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-024-253-2

Query Match   79.8%;  Score 595;  DB 1;  Length 136;
Best Local Similarity  82.9%;  Pred. No. 3e-53;
Matches 116;  Conservative 8;  Mismatches 10;  Indels 6;  Gaps 1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         ||||| |||||||||||||||||||||||||||||| ||||||||||||| || |||||
Db   1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVRLSCTASGFNIKDTYMHWVKQRP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||| ||||| ||||||| |||| ||||||  ||||||||||:||::
Db  61 EQGLEWIGRIDPANGNTKYDPRFQGKATIPADTSENTAYLQVNSLTSEDTAVYYCASGGN 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
         ||      ||||||| |||
Db 121 AW------LAYWGQGTLVTV 134
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RESULT 7
US-08-836-561-31
Sequence 31, Application US/08835561
Patent No. 6018032
GENERAL INFORMATION:
  APPLICANT: KOIKE, Masamichi
  APPLICANT: FURUYA, Akiko
  APPLICANT: NAKAMURA, Kazuyasu
  APPLICANT: IIDA, Akihiro
  APPLICANT: ANAZAWA, Hideharu
  APPLICANT: HANAI, Nobuo
  APPLICANT: TAKATSU, Kiyoshi
  TITLE OF INVENTION: Antibody Against Human Interleukin-5
  TITLE OF INVENTION: Receptor Alpha Chain
  NUMBER OF SEQUENCES: 106
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds LLP
    STREET: 1155 Avenue of the Americas
    CITY: New York
    STATE: NY
    COUNTRY: USA
    ZIP: 10036
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible

Right column

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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/836,561
  FILING DATE: 09-MAY-1997
  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 232384/95
  FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Lawrence, III, Stanton T
  REGISTRATION NUMBER: 25,736
  REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 212-790-9090
  TELEFAX: 212-869-9741
  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 137 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
US-08-836-561-31

Query Match   79.8%;  Score 593.5;  DB 3;  Length 137;
Best Local Similarity  82.9%;  Pred. No. 4.2e-53;
Matches 116;  Conservative 6;  Mismatches 13;  Indels 5;  Gaps 1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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Db   1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVNLSCTASGFNIKDTYMHWVKQRP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||| ||  |||| ||||  ||||||||||||||||||||||:||
Db  61 EQGLEWIGRIDPANGNTKSDPKFQGAKATIAADTSSNTAYLQLSSLTSEDTAVYYCT---- 116

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
          |      |||||| ||| 
Db 117 -GGLRLPFDVWGQGTLTV 135
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RESULT 8
US-08-561-521-17
Sequence 17, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
  APPLICANT: Bendig, Mary M.
  APPLICANT: Leger, Olivier J.
  APPLICANT: Saldanha, Jose
  APPLICANT: Jones, S. Tarran
  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
  TITLE OF INVENTION: Adhesion Molecule VLA-4
  NUMBER OF SEQUENCES: 45
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: One Market Plaza, Steuart Tower, Suite 2000
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94105
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC Compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/561,521
    FILING DATE:
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:

RESULT 9

PCT-US95-01219-17
Sequence 17, Application PC/TUS9501219
GENERAL INFORMATION:
  APPLICANT: Bendig, Mary M.
  APPLICANT: Leger, Olivier J.
  APPLICANT: Saldanha, Jose
  APPLICANT: Jones, S. Tarran
  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
    Adhesion Molecule VLA-4
  NUMBER OF SEQUENCES: 45
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: One Market Plaza, Steuart Tower, Suite 2000
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94105
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT/US95/01219
    FILING DATE: 25-JAN-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/186,269
    FILING DATE: 25-JAN-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Smith, William L.
    REGISTRATION NUMBER: 30,223
    REFERENCE/DOCKET NUMBER: 15270-14
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-543-9600
    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 142 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
PCT-US95-01219-17

Query Match   78.3%;   Score 584;   DB 2;   Length 142;
Best Local Similarity   77.1%;   Pred. No. 4.1e-52;
Matches 108;   Conservative 15;   Mismatches 17;   Indels 0;   Gaps 0;

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Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         : :| :|:| :|| : ||||| : |||:|| ||||: |||||||||||| |:| |
Db   1 MDWTWRVFCLLAVVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATIFADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
        |||:|||||||||||||||||||||:|| ||||:|||:||:|||:||||||::|||||
Db  61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
        ||||||||||||||||:|||
Db 121 YGNYGVYAMDYWGQGTLVTV 140
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APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Smith, William L.
  REGISTRATION NUMBER: 30,223
  REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-543-9600
  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 142 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-561-521-17

Query Match   78.3%;   Score 584;   DB 5;   Length 142;
Best Local Similarity   77.1%;   Pred. No. 4.1e-52;
Matches 108;   Conservative 15;   Mismatches 17;   Indels 0;   Gaps 0;

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Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         : :| :|:| :|| : ||||| : |||:|| ||||: |||||||||||| |:| |
Db   1 MDWTWRVFCLLAVVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATIFADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
        |||:|||||||||||||||||||||:|| ||||:|||:||:|||:||||||::|||||
Db  61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
        ||||||||||||||||:|||
Db 121 YGNYGVYAMDYWGQGTLVTV 140
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RESULT 10

US-08-561-521-44
Sequence 44, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
  APPLICANT: Bendig, Mary M.
  APPLICANT: Leger, Olivier J.
  APPLICANT: Saldanha, Jose
  APPLICANT: Jones, S. Tarran
  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
    Adhesion Molecule VLA-4
  NUMBER OF SEQUENCES: 45
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: One Market Plaza, Steuart Tower, Suite 2000
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94105
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/561,521
    FILING DATE:
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/186,269A
    FILING DATE: 25-JAN-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Smith, William L.
    REGISTRATION NUMBER: 30,223
    REFERENCE/DOCKET NUMBER: 15270-14
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-543-9600
    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 44:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 125 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-561-521-44

RESULT 11
Sequence 44, Application PC/TUS9501219
PCT-US95-01219-44
GENERAL INFORMATION:
    APPLICANT: Bendig, Mary M.
    APPLICANT: Leger, Olivier J.
    APPLICANT: Saldanha, Jose
    APPLICANT: Jones, S. Tarran
    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
    TITLE OF INVENTION: Adhesion Molecule VLA-4
    NUMBER OF SEQUENCES: 45
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Townsend and Townsend Khourie and Crew
        STREET: One Market Plaza, Steuart Tower, Suite 2000
        CITY: San Francisco
        STATE: California
        COUNTRY: USA
        ZIP: 94105
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: PCT/US95/01219
        FILING DATE: 25-JAN-1995
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/186,269
        FILING DATE: 25-JAN-1994
    ATTORNEY/AGENT INFORMATION:
        NAME: Smith, William L.
        REGISTRATION NUMBER: 30,223
        REFERENCE/DOCKET NUMBER: 15270-14
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 415-543-9600
        TELEFAX: 415-543-5043
    CLASSIFICATION:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 125 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
        MOLECULE TYPE: protein

  Query Match   75.3%; Score 562; DB 5; Length 125;
  Best Local Similarity 89.4%; Pred. No. 5.9e-50;
  Matches 110; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||||||||||||||||||||||||||:|:||||||||||||||||||| |||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYY--GNYGVYAMDYWGQGTS 137
         |||||||||||||||||||||||||||||||||||| || |||||| ||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGYYYYDSXVGYYAMDYWGQGTX 120

Qy 138 VTV 140
         |||
Db 121 VTV 123

RESULT 12
US-08-348-548-8
Sequence 8, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
    APPLICANT: Berdoz, Jose
    APPLICANT: Kraehenbuhl, Jean Pierre
    TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
    TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
    NUMBER OF SEQUENCES: 108
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Fish & Richardson
        STREET: 225 Franklin Street, Suite 3100
        CITY: Boston
        STATE: MA
        COUNTRY: USA
        ZIP: 02110-2804
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS,
        SOFTWARE: PatentIn Release #1.0, Version #1.30B
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/348,548
        FILING DATE: 01-DEC-1994
    ATTORNEY/AGENT INFORMATION:
        NAME: Clark, Paul T.
        REGISTRATION NUMBER: 30,162
        REFERENCE/DOCKET NUMBER: 06132/009001
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (617) 542-5070
        TELEFAX: (617) 542-5070
        TELEX: 200154
    INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 136 amino acids
        TYPE: amino acid
        STRANDEDNESS: not relevant
        TOPOLOGY: linear
        MOLECULE TYPE: protein
US-08-348-548-8

  Query Match   74.3%; Score 554; DB 4; Length 136;
  Best Local Similarity 80.7%; Pred. No. 4.3e-49;
  Matches 113; Conservative 6; Mismatches 15; Indels 6; Gaps 3;

Qy   1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         |||||:|:||||||||||||||||||||||||||||||| |||||||||:|| |||||||
Db   1 MKCSWVIFFLMAVVT-VNSEVQLQQSGAELVKPGALVKLSCKASGFNIKDIYMWYWVKQRP 59

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||||||||||||| |||||||||||||||||||||||||||||||||||:||:|
Db   60 EQGLEWIGWIDPENGNTVYDPKFQGKASITADTSSNTAYLQLSSLLASEDTAVYYCA---Y 116

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
         || ||||||||||||| |||
Db 117 YGT--SYWFYWGQGTLVTV 134

RESULT 13
PCT-US95-15716-8
Sequence 8, Application PC/TUS9515716
GENERAL INFORMATION:
    APPLICANT: Berdoz, Jose

APPLICANT: Kriehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15716
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06137/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15716-8

Query Match   74.38;   Score 554;   DB 5;   Length 136;
Best Local Similarity 80.7%;   Pred. No. 4.3e-49;
Matches 113;   Conservative 6;   Mismatches 15;   Indels 6;   Gaps 3;

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Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
         |||||| |||||||| || |||||||||||||| ||| |||| ||||||| |  ||||||
Db   1 MKCSWVIFFLMAVVT-VNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRP  59

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKRATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||| ||| || | |||||||| ||| ||||||||||||||||| |||||| |
Db  60 EQGLEWIGWIDPENGNTVYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYCA--Y 116

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
        || |||||||| |||
Db 117 YGT--SYWFPYWGQGTLVTV 134
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RESULT 14
US-08-561-521-11
Sequence 11, Application US/08561521
GENERAL INFORMATION:
Patent No. 5840299
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-11

Query Match   72.98;   Score 544;   DB 2;   Length 123;
Best Local Similarity 82.6%;   Pred. No. 3.9e-48;
Matches 100;   Conservative 11;   Mismatches 10;   Indels 0;   Gaps 0;

```
Qy  20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
        :||| |||||| | |||||||:|| |||||||||||||||  | :|: |||||||||||||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60

Qy  80 DPKFQGKRATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
        |||||| :|||||||:  :||||:|:||||||||||:|||||||||||||||||||||| |
Db  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy 140 V 140
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Db 121 V 121
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RESULT 15
PCT-US95-01219-11
Sequence 11, Application PCT/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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~ ;   APPLICATION NUMBER:  PCT/US95/01219
~ ;   FILING DATE:  25-JAN-1995
~ ;   CLASSIFICATION:
~ ;   PRIOR APPLICATION DATA:
~ ;   APPLICATION NUMBER:  US 08/186,269
~ ;   FILING DATE:  25-JAN-1994
~ ;   ATTORNEY/AGENT INFORMATION:
~ ;   NAME:  Smith, William L.
~ ;   REGISTRATION NUMBER:  30,223
~ ;   REFERENCE/DOCKET NUMBER:  15270-14
~ ;   TELECOMMUNICATION INFORMATION:
~ ;   TELEPHONE:  415-543-9600
~ ;   TELEFAX:  415-543-5043
~ ;   TELEPHONE:  415-543-5043
INFORMATION FOR SEQ ID NO:  11:
~ ;   SEQUENCE CHARACTERISTICS:
~ ;   LENGTH:  123 amino acids
~ ;   TYPE:  amino acid
~ ;   STRANDEDNESS:  single
~ ;   TOPOLOGY:  linear
~ ;   MOLECULE TYPE:  protein
PCT-US95-01219-11
```

```
Query Match           72.98;   Score 544;   DB 5;   Length 123;
Best Local Similarity  82.6%;   Pred. No. 3.9e-48;
Matches 100;  Conservative 11;  Mismatches 10;  Indels 0;  Gaps 0;

Qy   20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY   79
         :|||  |||||:  |||||||| :||  ||||||||||:|  ||||  |:||||||||||||
Db    1  QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY   60

Qy   80  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT  139
         ||||||:  |||||||||:||:|||  |||||||||||||||||||||||||||||| ||
Db   61  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT  120

Qy  140  V  140
         |
Db  121  V  121
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Search completed: May 7, 2002, 12:23:04
Job time: 175 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:47 ; Search time 37.68 seconds
                                          (without alignments)
                                          283.026 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_68:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Title:
Perfect score: 746
Sequence: 1 MKCSWVMFLMAAVTGVNSE.........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	603.5	80.9	178	2	S29594	Ig gamma chain (WM
2	597	80.9	136	2	S04576	Ig heavy chain pre
3	570.5	76.5	137	2	S52445	Ig heavy chain V r
4	567.5	76.1	137	2	PHI403	Ig heavy chain V r
5	539	72.3	123	2	S03471	Ig heavy chain V-D
6	523	70.1	120	2	S17586	Ig heavy chain V-D
7	521.5	69.9	117	2	S06823	Ig heavy chain V r
8	515	69.0	122	2	S03482	Ig heavy chain V-D
9	500	67.0	115	2	S24289	Ig ganma chain V r
10	498	66.8	116	2	S03484	Ig heavy chain V-D
11	494.5	66.3	120	2	A56446	Ig heavy chain V r
12	493.5	66.2	108	2	PHI012	Ig heavy chain V r
13	492	66.0	221	2	S49220	ganma-1 chain -
14	472.5	63.3	114	4	A47271	nitrophenyl phosph
15	471	63.1	140	2	PHI482	Ig heavy chain V r
16	467	62.6	107	2	PHI013	Ig heavy chain V r
17	466.5	62.6	139	2	PS0024	Ig heavy chain pre
18	464.5	62.3	139	1	MHMS18	Ig heavy chain V r
19	462.5	62.0	99	2	D37262	Ig heavy chain V r
20	461.5	61.9	115	2	PI0246	Ig heavy chain pre
21	461.5	61.9	139	2	A27609	Ig heavy chain V r
22	460.5	61.7	141	2	JL0076	Ig heavy chain pre
23	459	61.5	135	2	PHI492	Ig heavy chain V r
24	459	61.5	140	1	HVMSG7	Ig heavy chain V r
25	457.5	61.3	107	2	A27646	Ig heavy chain V r
26	457	61.3	138	2	E32513	Ig heavy chain V r
27	456	61.1	249	2	S41374	single chain Fv an
28	455.5	61.1	141	2	A39276	Ig heavy chain pre
29	455	61.0	140	2	PHI498	Ig heavy chain V r
30	454.5	60.9	133	2	PC1155	Ig heavy chain pre
31	454	60.9	118	2	S25174	Ig heavy chain V r
32	454	60.9	138	2	S21810	Ig heavy chain V r
33	453	60.7	140	2	PHI484	Ig heavy chain V r
34	452	60.6	135	2	PHI493	Ig heavy chain V r
35	451.5	60.5	469	2	S37483	Ig ganma-2a chain
36	451	60.5	135	2	PHI494	Ig heavy chain V r
37	447	59.9	140	2	PHI489	Ig heavy chain V r
38	444	59.5	140	2	PHI486	Ig heavy chain V r
39	441	59.1	140	2	PHI488	Ig heavy chain V r
40	440.5	59.0	120	2	S20643	Ig gamma chain -
41	440	59.0	122	2	S38950	Ig ganma chain V r
42	440	59.0	246	2	S40295	Ig gamma-2a chain
43	440	59.0	446	2	S20646	Ig heavy chain V r
44	439	58.8	123	2	C37262	Ig heavy chain V r
45	438	58.7	99	2		

ALIGNMENTS

RESULT   1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match   80.9%; Score 603.5; DB 2; Length 178;
Best Local Similarity   88.1%; Pred. No. 1.5e-45;
Matches 118; Conservative 6; Mismatches 5; Indels 5; Gaps 2;

Qy   7 MFFLMAAVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEW 66
            :||||||||||||||||||||||||||||||||||||||||||:||||||:|||||||
Db   1 IFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEW 60

Qy   67 IGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGV 126
           |||||||||||:||||:||||||||||:|||||||||||||||||||| |||
Db   61 IGRIDPANGYTEYDPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG---GNY-A 115

Qy   127 YAMDYWGQGTSVTV 140
          ||||||||||||||
Db   116 YGMDYWGQGTSVTV 129

RESULT   2
S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involv
A;Reference number: S04573; MUID:87133856
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>

```
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match     80.0%;   Score 597; DB 2;  Length 136;
Best Local Similarity 82.9%;   Pred. No. 4.1e-45;
Matches 116;  Conservative 6;  Mismatches 12;  Indels 6;  Gaps 1;

Qy    1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||||| |||||||| :||||||||||||||||:||||||||||||||||| ::| |||||
Db    1 MKCSWIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDYMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||| ||||  | || :|||||||:|||||||| |||||||||||||||||: :
Db   61 EQGLEWIGWIDPENGDTQYASKFQGKATMTADTSSNTTYLQLSSLTSEDTAVYYCI--- 116

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
          |:| ||||||||||||||||
Db  117 --TYGAYAMDYWGQGTSVTV 134
```

RESULT 3
S52445
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995
C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
A;Description: submitted to the EMBL Data Library, November 1994
A;Reference number: S52445
A;Accession: S52445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>

```
Query Match     76.5%;   Score 570.5; DB 2;  Length 137;
Best Local Similarity 81.4%;   Pred. No. 8.4e-43;
Matches 114;  Conservative 6;  Mismatches 15;  Indels 5;  Gaps 2;

Qy    1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          ||||| ||||||||||||||||||||||||:|||:||||| :|||||||||:: | |||||
Db    1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYIMWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          ||||||| |||||| |  |||||||||:||||||||||||||||| :||||||||||
Db   61 EQGLEWIGWIDPENGTIVYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 117

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
          ||| ::| |||||||| ||
Db  118 YGT--SYWPYWGQGTLVTV 135
```

RESULT 4
PH1403
Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: PH1403
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
ia virus.,
A;Reference number: PH1403; MUID:93018837
A;Accession: PH1403
A;Molecule type: DNA
A;Residues: ,1#123 <SHI>

C;Genetics:
C;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>

```
Query Match     76.1%;   Score 567.5; DB 2;  Length 123;
Best Local Similarity 94.9%;   Pred. No. 1.4e-42;
Matches 111;  Conservative 3;  Mismatches 2;  Indels 1;  Gaps 1;

Qy    1 MKCSWVWFFLMAVVT-GVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQR 59
          ||||| ||||||||| |||||||||||||||||||||||||||||||||||:: | |||||
Db    1 MKCSWIFFLMAVVTAGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDYMHWVKQR 60

Qy   60 PEQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||:||
Db   61 PEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA 117
```

RESULT 5
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match     72.3%;   Score 539; DB 2;  Length 120;
Best Local Similarity 89.3%;   Pred. No. 4e-40;
Matches 108;  Conservative 2;  Mismatches 7;  Indels 4;  Gaps 1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          |||||||||||||||||||||||||||||||||:| ||||||||||||||||||||| |||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYGNYGVYAMDYWGQGTSVT 139
          ||||||||||||||||||||||||||||||||||:|||    |: :| |||||||||||||
Db   61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR----GWLRRDAMDYWGQGTSVT 116

Qy  140 V 140
          |
Db  117 V 117
```

RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991

A;Title: Biochemical implications from the variable gene sequences of an anti-cytochrome
forms.
A;Reference number: S17586; MUID:92015240
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
A;Superfamily: immunoglobulin V region; immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match    70.1%;  Score 523; DB 2; Length 117;
Best Local Similarity    85.2%;  Pred. No. 9.6e-39;
Matches 104; Conservative   7; Mismatches   3; Indels   8; Gaps   3;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         ||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||:||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY-YGNYGVYAMDYWGQGTSV 138
         ||||| ||||||||||||||| ||||||||||||| || ::   ||||:     ||||| ::
Db   61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113

Qy  139 TV 140
         ||
Db  114 TV 115
```

RESULT   7
S06823
Ig heavy chain V region (clone IIc) - mouse
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin
J;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp...
A;Reference number: S06815; MUID:90064531
A;Accession: S06823
A;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
A;Species: Mus musculus (house mouse)

```
Query Match    69.9%;  Score 521.5; DB 2; Length 122;
Best Local Similarity    86.9%;  Pred. No. 1.4e-38;
Matches 106; Conservative   4; Mismatches   9; Indels   3; Gaps   3;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIH-CVKQRPEQGLEWIGRIDPANGYTK 78
         |||||||||||||||||||||||||||||||||||| |:|||||||||||||||||||||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTK 60

Qy   79 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
         :||||||||||||||||||||| |||||||||||| ||: |||||||||
Db   61 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR-GWL-RRDAMGVDYWGQGTSV 118

Qy  139 TV 140
         ||
Db  119 TV 120
```

RESULT   8
S03482
Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
A;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453

R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03482
A;Accession: S03471; MUID:84057768
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Mohier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug...
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match    69.0%;  Score 515; DB 2; Length 115;
Best Local Similarity    83.5%;  Pred. No. 4.7e-38;
Matches 101; Conservative   4; Mismatches  10; Indels   6; Gaps   1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         |||||||||||||||||||||||||||||||||||:| ||||||||||||||||||:||
Db    1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
         ||||||||||||||||||||| |||||||||||| ||:
Db   61 DPKFQGKATITADTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR-----DVWGQGTTL 114

Qy  140 V 140
         |
Db  115 V 115
```

RESULT   9
S24289
Ig gamma chain V region (J334/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: S24287
A;Accession: S24289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;14-97/Domain: immunoglobulin homology <IMM>

```
Query Match    67.0%;  Score 500; DB 2; Length 116;
Best Local Similarity    81.0%;  Pred. No. 9.5e-37;
Matches  98; Conservative   9; Mismatches   6; Indels   8; Gaps   2;

Qy   21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
         |||||||||||||||||||||||||||||||||||:| ||||:|||||||||||:||:|||
Db    1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60

Qy   81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EGYYGNYGVYAMDYWGQGTSVT 139
         ||||||||||||||||||||| |||||||||||| ||  :|||
Db   61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARAGYY-----FDYWGQGTLT 113

Qy  140 V 140
         |
Db  140 V 140
```

RESULT 10
S03484

Db   114 V 114

A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
A;Accession: S03484
C;Accession: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453
A;Accession: S07453; MUID:83058021
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology

Query Match   66.8%;   Score 498;   DB 2;   Length 120;
Best Local Similarity   82.6%;   Pred. No. 1.5e-36;
Matches 100;   Conservative   5;   Mismatches 12;   Indels 4;   Gaps 1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
              ||||||||||||||||||||||||||||| ||||||||||||||||||:| ||||||||
Db   1 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGIYGNGVYAMDYWGQGTSVT 139
              |||||||||||||||:|||||||||||||||||||||||:|:||| ||||||||||||
Db   61 GPKFQGKATITADTSSSAAYLQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116

Qy   139 TV 140
              ||
Db   117 TV 118

RESULT 11
A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi
A;Reference number: A56446; MUID:95229583
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match   66.3%;   Score 494.5;   DB 2;   Length 268;
Best Local Similarity   80.3%;   Pred. No. 6.8e-36;
Matches   98;   Conservative   8;   Mismatches 11;   Indels 5;   Gaps 2;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

RESULT 12
PH1012

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
Ig heavy chain V region (clone 17p.73) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Reference number: PH0971; MUID:92381444
A;Accession: PH1012
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   66.2%;   Score 493.5;   DB 2;   Length 108;
Best Local Similarity   85.8%;   Pred. No. 3.3e-36;
Matches   97;   Conservative   3;   Mismatches   8;   Indels 5;   Gaps 1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
              ||||||||||||||||||||||||||||| ||||||||||||||||||:| ||||||||
Db   1 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGIYGNGVYAMDYW 132
              |||||:||||||||||||||||||||||||||||||||| ||||
Db   61 APKFQDKRATITADTSSNTAYLQLSSLTSEDTAVYYCARRDNY----YAMDYW 108

RESULT 13
S49220

Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A;Reference number: S49220
A;Accession: S49220
A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match   66.0%;   Score 492;   DB 2;   Length 221;
Best Local Similarity   79.3%;   Pred. No. 9.2e-36;
Matches   96;   Conservative   8;   Mismatches 13;   Indels 4;   Gaps 1;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

```
Db        1  QVKLLESGAELVKSGASVKLSCTASGFNIKDTYIHWVKQRPEQGLEWIGRIDPANGEIKY  60
             | |:|:||||||| |||||||||||||||||||||||||||||||||||||||||||| ||

Qy       80  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT  139
             |||||| |||||||||||||||||||||||||||||||||||||||||||||||::|
Db       61  DPKFQGTATITADTSNTAYLQLSSLTSEDTAVYYCVRRG------YGSSQEPYWGQGTTLT  116

Qy      140  |
        117 V 140
Db      117 V 117
```

RESULT 14
A47271
nitrophenyl phosphonate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)
C;Species: synthetic
A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
C;Accession: A47271
R;Lesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic acti
A;Reference number: A47271; MUID:93165660
A;Accession: A47271
A;Molecule type: DNA; protein
A;Residues: 1-114 <LES>
A;Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A;Note: parts of this sequence were determined by protein sequencing
F;22-96/Disulfide bonds: #status predicted

```
Query Match            63.3%;  Score 472.5;  DB 4;  Length 114;
Best Local Similarity   77.7%;  Pred. No. 2.3e-34;
Matches     94;  Conservative    8;  Mismatches   10;  Indels   9;  Gaps    2;

Qy       20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
             :|:| ::||||||||||||||||||||||||||: ||||:||||||||||||||||| ||
Db        1  QVKLLESGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKY  60

Qy       80  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT  139
             |||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       61  DPKFQDKATITADTSSKTVIQLSGLTSEDTAVYYCA--SYYG-------IYWGQGTTLT  111

Qy      140  |
        112 V 140
Db      112 V 112
```

RESULT 15
PH1482
Ig heavy chain V region (clones 36-35[TG] and X7-TG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A;Reference number: PH1482; MUID:93171820
A;Accession: PH1482
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Experimental source: hybridoma cell
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

```
Query Match            63.1%;  Score 471;  DB 2;  Length 140;
Best Local Similarity   65.0%;  Pred. No. 3.8e-34;
```

```
Matches     91;  Conservative   19;  Mismatches   28;  Indels   2;  Gaps    1;

Qy        1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
             |    |:: |:|| |:|:||||||||||||||||||| |:|||||||| |:|||||||
Db        1  MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP  60

Qy       61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY  120
             | ||||||||| ||||||||:: | |||||||||||||||||||||||||||||||||| |
Db       61  GQGLEWIGYINPGNGYTKYNEKFKGKTTLTVDKSSSTAYMQLRSLISEDSAVYFCARSVY  120

Qy      121  YGNYGVYAMDYWGQGTSVTV  140
             |:| |||||||||||| :||
Db      121  YG--GSYYFDYWGQGTTLTV  138
```

Search completed: May 7, 2002, 12:23:47
Job time: 198 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:34 ; Search time 21.92 Seconds
                                              (without alignments)
                                              234.173 Million cell updates/sec

Title:
Perfect score: 746
Sequence: 1 MKCSWVWFFLMAAVTGVNSE..........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
                       Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                       Maximum Match 100%
                       Listing first 45 summaries

Database :   SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	464.5	62.3	139	1	HV07_MOUSE	P01751	mus musculu
2	459	61.5	140	1	HV02_MOUSE	P01746	mus musculu
3	425	57.0	120	1	HV03_MOUSE	P01747	mus musculu
4	422.5	56.6	137	1	HV11_MOUSE	P01755	mus musculu
5	416	55.8	138	1	HV48_MOUSE	P03980	mus musculu
6	411	55.1	117	1	HV09_MOUSE	P01753	mus musculu
7	396	53.1	136	1	HV15_MOUSE	P01759	mus musculu
8	393	52.7	117	1	HV06_MOUSE	P01750	mus musculu
9	393	52.7	117	1	HV49_MOUSE	P06328	mus musculu
10	389	52.1	117	1	HV10_MOUSE	P01754	mus musculu
11	388	52.0	117	1	HV04_MOUSE	P01748	mus musculu
12	381	51.1	117	1	HV52_MOUSE	P06327	mus musculu
13	379	50.8	117	1	HV13_MOUSE	P01757	mus musculu
14	379	50.8	121	1	HV01_MOUSE	P01745	mus musculu
15	378.5	50.7	147	1	HV1C_HUMAN	P01744	homo sapien
16	374	50.1	117	1	HV05_MOUSE	P01749	mus musculu
17	374	50.1	117	1	HV12_MOUSE	P01756	mus musculu
18	372	49.9	117	1	HV14_MOUSE	P01758	mus musculu
19	368.5	49.4	117	1	HV51_MOUSE	P06330	mus musculu
20	367	49.2	118	1	HV1B_HUMAN	P06329	homo sapien
21	360.5	48.3	120	1	HV50_MOUSE	P06329	mus musculu
22	359	48.1	117	1	HV1G_HUMAN	P23083	homo sapien
23	356.5	47.8	136	1	HV16_MOUSE	P01783	mus musculu
24	321.5	43.1	114	1	HV00_MOUSE	P01741	mus musculu
25	316.5	42.4	119	1	HV38_MOUSE	P01808	mus musculu
26	315	42.2	117	1	HV42_MOUSE	P01812	mus musculu
27	314	42.1	117	1	HV1A_HUMAN	P01742	homo sapien
28	312.5	41.9	117	1	HV37_MOUSE	P01807	mus musculu
29	311	41.7	142	1	HV01_RAT	P01744	rattus norv
30	310.5	41.6	119	1	HV40_MOUSE	P01810	mus musculu
31	304	40.8	118	1	HV39_MOUSE	P01809	mus musculu
32	297	39.8	137	1	HV46_MOUSE	P01822	mus musculu
33	297	39.8	144	1	HV26_MOUSE	P01795	mus musculu
34	293.5	39.3	120	1	HV1H_HUMAN	P80421	homo sapien
35	292	39.1	117	1	HV41_MOUSE	P01811	mus musculu
36	291.5	39.1	116	1	HV05_CARAU	P19181	carassius a
37	290	38.9	116	1	HV36_MOUSE	P01806	mus musculu
38	290	38.9	123	1	HV24_MOUSE	P01793	mus musculu
39	288	38.6	117	1	HV3C_HUMAN	P01764	homo sapien
40	285.5	38.3	116	1	HV3T_HUMAN	P01781	homo sapien
41	284.5	38.1	122	1	HV43_MOUSE	P01768	mus musculu
42	284	38.1	144	1	HV3G_HUMAN	P01819	homo sapien
43	284	38.1	116	1	HV2I_HUMAN	P01769	homo sapien
44	282.5	37.9	122	1	HV3A_HUMAN	P06331	homo sapien
44	282.5	37.9	122	1	HV1F_HUMAN	P01762	homo sapien
45	282	37.8	125	1	HV1F_HUMAN	P06326	homo sapien

ALIGNMENTS

RESULT 1
HV07_MOUSE

ID   HV07_MOUSE   STANDARD;   PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC   MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC   (NPB ANTIBODIES).
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A02034; MHMS18.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   139   IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN   20   49   FRAMEWORK 1.
FT   DOMAIN   50   54   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   55   68   FRAMEWORK 2.
FT   DOMAIN   69   85   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   86   117   FRAMEWORK 3.
FT   DOMAIN   118   124   D SEGMENT.
FT   DOMAIN   125   139   JH2 SEGMENT.
FT   NON_TER   1
FT   DISULFID   41   115   BY SIMILARITY.
SQ   SEQUENCE   139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match   62.3%;   Score 464.5; DB 1; Length 139;
Best Local Similarity   65.0%;   Pred. No. 8.1e-38;

```
Matches  91; Conservative  18; Mismatches  28; Indels   3; Gaps   1;

Qy    1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        ||||| |||||| :| |||:|||||| ||||||||||||||:||| | :||:| |||||
Db    1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
        ||||||||||:|: ||:|||:||||||||:|:||||||||||||||||||:||| :||
Db   61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
        || |   ||:||||||:::||
Db  121 YGS---SYFDYWGQGTTLTV 137
```

RESULT   2
ID   HV02_MOUSE   STANDARD;   PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; 1g; 1.
DR   SMART; SM00406; Igv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   140
FT   NON_TER   140   140
SQ   SEQUENCE   140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match   63.6%; Score 459; DB 1; Length 140;
Best Local Similarity   61.5%;
Matches 89; Conservative 18; Mismatches 31; Indels   2; Gaps   1;

Qy   1 MKCSWVWFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        |:|| ||||:||| ||:|||||||||||||||||||||| :|| | |||:||||||||
Db   1 MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
        |||||||| :|||||:||| ||| |||| | ||||||: | |||:||||||||||| |
Db   61 GQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHY 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
        || | ||:|||||:||||
Db 121 YG--GSYFDFDYWGQGTPLTV 138
```

RESULT   3
ID   HV03_MOUSE   STANDARD;   PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC   DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC   CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC   SEGMENT, JH2.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; 1g; 1.
DR   SMART; SM00406; Igv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT   NON_TER   120   120
SQ   SEQUENCE   120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match   68.3%; Score 425; DB 1; Length 120;
Best Local Similarity   57.0%;
Matches 82; Conservative 14; Mismatches 22; Indels   2; Gaps   1;

Qy   21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
        ||||||||||: | |||:|| ||| | : |:||||| |:|||||||||:|||| ||:
Db   1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy   81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
        ||| | : | | ||||||| | ||:|| ||||||| || | |:| :|||| ||
Db   61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYG--GSYFDYWGQGTTLTV 118
```

RESULT   4
ID   HV11_MOUSE    STANDARD;    PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NpB family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
```

```
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    122       D SEGMENT.
FT   DOMAIN      123    137       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     137    137
SQ   SEQUENCE    137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;

Query Match             56.6%;  Score 422.5;  DB 1;  Length 137;
Best Local Similarity   61.4%;  Pred. No. 8.4e-34;
  Matches   86;  Conservative   16;  Mismatches   33;  Indels   5;  Gaps  2;

Qy         1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
             | | |||  || | |||| |||||| ||| |||||||||| |  : || |||
Db         1 MGWSCIMLFLAATATGVHSQVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRP 60

Qy        61 EQGLEWIGRIDPANGYTRKYDPKFQGKAITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
             : |||||| |:|:|:  ||:|  :  ||  :|||||||||||||||:||:||:|
Db        61 GRGLEWIGRIDNSGGTTYNEHPRSKAILTIDKPSSTAYMQLSSLTSEDSAVYYCARY-R 119

Qy       121 YGNYGVYAMDYWGQGTSVTV 140
             |||||||:|:||
Db       120 LGRY---FDYWGQGTLTV 135
```

```
RESULT   5
HV48_MOUSE      STANDARD;      PRT;     138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN       21     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    127       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      128    138       FRAMEWORK 4.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     138    138
SQ   SEQUENCE    138 AA;  15576 MW;  748157E4C6907B8E CRC64;

Query Match             55.8%;  Score 416;  DB 1;  Length 138;
Best Local Similarity   60.0%;  Pred. No. 3.6e-33;
  Matches   84;  Conservative   21;  Mismatches   29;  Indels   6;  Gaps  2;

Qy         1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
             | | || |:|| : ||||:|||||| |||:||||||| ||| |:||||||:||:||
Db         1 MGWSIILFLVATADVHSQVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHHWVKQRP 60

Qy        61 EQGLEWIGRIDPANGYTRKYDPKFQGKAITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 119
             |||||| |:|:|:  ||:|  :  ||  :||||||||| | :||:||:|
Db        61 GQGLEWIGEINPDGRSNYNEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDG 120

Qy       120 YGNYGVYAMDYWGQGTSVT 139
             ||  |||:|:||
Db       121 YYDWF-----VYWGQGTLVT 135
```
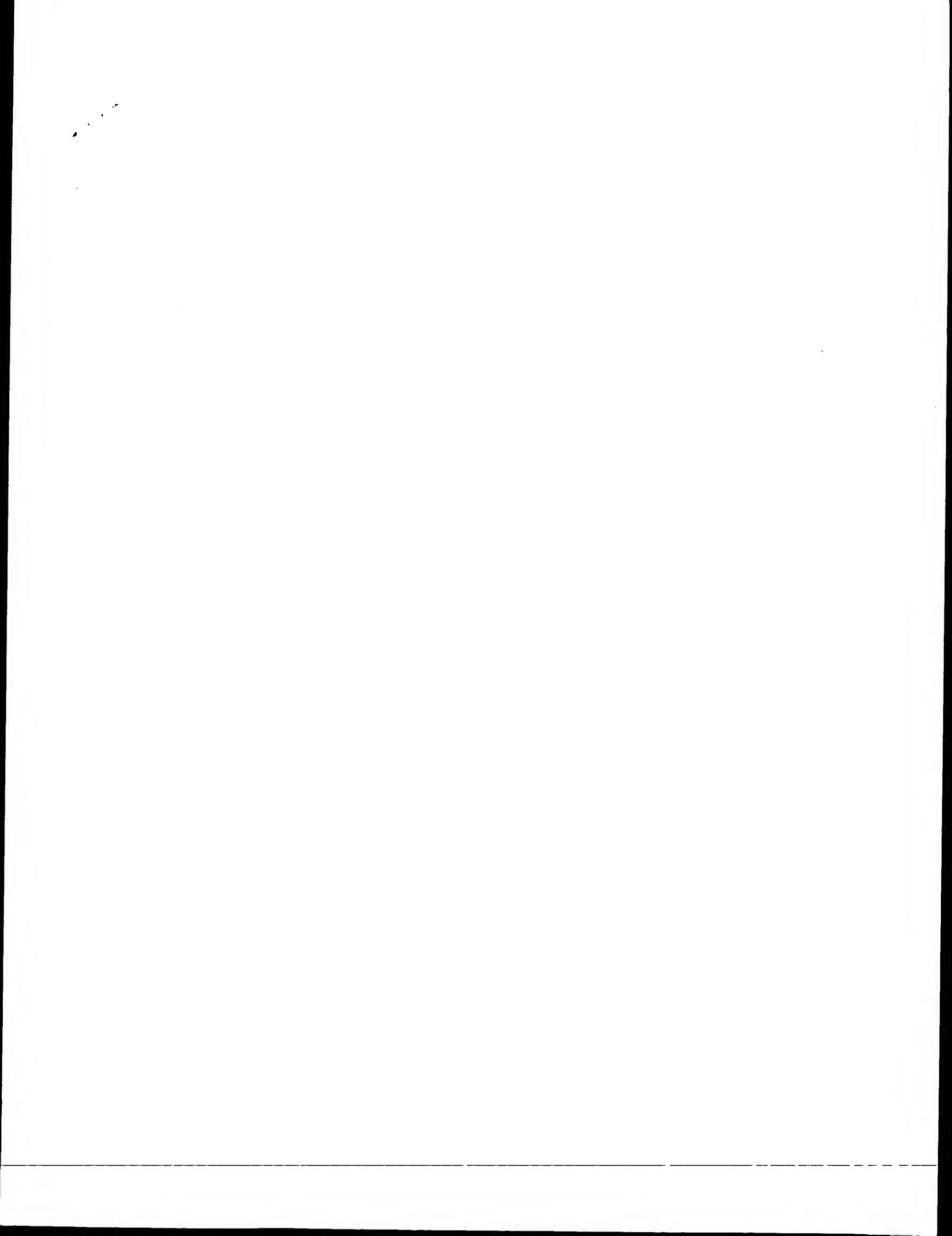
```
RESULT   6
HV09_MOUSE      STANDARD;      PRT;     117 AA.
AC   P01753; P11271;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NpB family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; B02034; HVMS61.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 186-1.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;  12890 MW;  16191A088CB17F5A CRC64;

Query Match             55.1%;  Score 411;  DB 1;  Length 117;
Best Local Similarity   68.4%;  Pred. No. 8.9e-33;
```

Matches   80; Conservative   15; Mismatches   22; Indels   0; Gaps   0;

```
Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         | .||| :|| | ||:|:||:|||:||||||||||||  :|| ||||
Db   1 MGWSCIIFFLAAFATATGVHSQVQLQQPGAELVKPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
         ||||||||||||:||:||| |::|||||| ||:|:|||||||||||||||||||||||
Db  61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCAR 117
```

RESULT 7
HV15_MOUSE

ID   HV15_MOUSE   STANDARD;   PRT;   136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT   by two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).

DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   136   IG HEAVY CHAIN V REGION BCL1.
FT   NON_TER   136   136
SQ   SEQUENCE   136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match   53.1%; Score 396; DB 1; Length 136;
Best Local Similarity 55.7%; Pred. No. 2.9e-31;
Matches   78; Conservative   23; Mismatches   33; Indels   6; Gaps   2;

```
Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         | .||| :|| | ||:|:||:|||:|||||||||||||  :|| ||:|  :| ||||||
Db   1 MGWSCIIFFLVATATGVHSQVQLQQPGAEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSH 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||||| | :|  |:| |  |||| | :| ::|:|| ||:||:||:  |:|| | |
Db  61 AKSLEWIGVISTINGNTSYNQKFKGKATMTVDKSSSTVHMELARITSEDSANLYCAR--Y 118

Qy 121 YGNYGVYAMDYWGGGTSVTV 140
         |:| |  | || |||:|:|
Db 119 YGNY---FDYWGGGTLLTV 134
```

RESULT 8
HV06_MOUSE

ID   HV06_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01750;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NpB family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC   RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02032; HVMS02.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   117   IG HEAVY CHAIN V REGION 102.
FT   DOMAIN   20   49   FRAMEWORK 1.
FT   DOMAIN   50   54   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   55   68   FRAMEWORK 2.
FT   DOMAIN   69   85   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   86   117   FRAMEWORK 3.
FT   DISULFID   41   115   BY SIMILARITY.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match   52.7%; Score 393; DB 1; Length 117;
Best Local Similarity 65.5%; Pred. No. 4.8e-31;
Matches   76; Conservative   17; Mismatches   23; Indels   0; Gaps   0;

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Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
         | .||| :|| | ||:|:||:||||||||||||||||||  :|| ||:|  :| ||||||
Db   1 MGWSCIIFFLVAFATGVHSHVQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRP 60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
         |||||||||| | :||  |:|||||||| | :| :::|:|||||||||||:|||||
Db  61 GQGLEWIGRIHPSDSDTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116
```

RESULT 9
HV49_MOUSE

ID   HV49_MOUSE   STANDARD;   PRT;   117 AA.
AC   P06328;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration

```
DR   EMBL; M13788; AAA38506.1; -.
DR   PIR; A02035; MHMSB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION VH558 B4.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;   12834 MW;  B8862FAC67ABD345 CRC64;

Qy   1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        | ||| ||||  || |  ||||||||||||||||||||||||||||||:| ||||
Db   1  MGWSCIMLFLAATATGVHSPVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy  61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
        :||||||| |||| :| ||| ||: ||  ||:||||||||||||||||::| ||
Db  61  GRGLEWIGNIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCTR 117

Query Match             52.7%;  Score 393; DB 1; Length 117;
Best Local Similarity   65.8%;  Pred. No. 4.8e-31;
Matches   77; Conservative  14; Mismatches  26; Indels   0; Gaps   0;
```

```
RESULT 10
HV10_MOUSE
ID   HV10_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01754; P11270;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 145 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
```

```
DR   EMBL; J00533; AAA36602.1; -.
DR   PIR; C02034; HVMS45.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 145.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;   12921 MW;  D37DE8A3F5A3E996 CRC64;

Qy   1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        | ||| ||||  || |  ||||||||||||||||||||||||||||||:| ||||
Db   1  MGWSCIMLFLAATATGVHSPVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy  61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
        :||||||||  |||| :| ||| ||: ||  ||:||||||||||||||::| ||
Db  61  GRGLEWIGNIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR 117

Query Match             52.1%;  Score 389; DB 1; Length 117;
Best Local Similarity   65.8%;  Pred. No. 1.1e-30;
Matches   77; Conservative  15; Mismatches  25; Indels   0; Gaps   0;
```

```
RESULT 11
HV04_MOUSE
ID   HV04_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01748;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02030; HVMS23.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 23.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;   12772 MW;  C530F829C906F69B CRC64;

Qy   1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
        | ||| ||||  || |  ||||||||||||||||||||||||||||||:| ||||
Db   1  MGWSCIMLFLAATATGVHSPVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy  61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
        :||||||||||||  :| ||| ||: ||  ||:||||||||||||||::| ||
Db  61  GRGLEWIGRIDPDNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR 117

Query Match             52.0%;  Score 388; DB 1; Length 117;
Best Local Similarity   64.1%;  Pred. No. 1.4e-30;
Matches   75; Conservative  15; Mismatches  27; Indels   0; Gaps   0;
```

```
Qy   1 MKCSWVWFFLMAVVTGVNSEVOLQQSGASVKLSCTASGFNIKDTYIHCVKRQRP          60
         :|::||  |:||    ||||||||        |||:|  |::|  | |||:|
Db   1 MGWSCIILFLVAAANGVHSQVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQPG   60

Qy  61 EQGLEWIGRIDPANGYTKYDPKFQGKRATITADTSSNTAYLQLSSLTSEDTAVYFCAR    117
        |::|| ||||| |:| |:||  |||||:|| |:|||||||||::|||:||||||||
Db  61 GQGLEWIGNINPGGNGGTNYNEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR     60
```

RESULT 12

```
ID   HV52_MOUSE     STANDARD;      PRT;   117 AA.
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; M13787; AAA38499.1; -.
DR   PIR; A02029; HVMSA1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION VH558 A1/A4.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12971 MW;  8B0BC138856DFC9D CRC64;
```

Query Match   51.1%; Score 381; DB 1; Length 117;
Best Local Similarity   65.5%; Pred. No. 6.7e-30;
Matches   74; Conservative 16; Mismatches 23; Indels   0; Gaps   0;

```
Qy   5 WVWFFLMAVVTGVNSEVOLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL   64
         |:|  |::|    ||| :|:|| ||||||| |:|  |::|  | |||:|  |||||:|||
Db   5 WIFLFLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGL    64

Qy  65 EWIGRIDPANGYTKYDPKFQGKRATITADTSSNTAYLQLSSLTSEDTAVYFCAR       117
        ||||  | |:| |:||  |:|||||:|| |:|||||||||::|||:|||||||
Db  65 EWIGWIYPGDGSTKYNEKFKGKRATLTADKSSSTAYMQLSSLTSENSAVYFCAR       117
```

RESULT 13

```
ID   HV13_MOUSE     STANDARD;      PRT;   117 AA.
```

```
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC       WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A26242; MHMSJ5.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13024 MW;  292E2AF4BE447E41 CRC64;
```

Query Match   50.8%; Score 379; DB 1; Length 117;
Best Local Similarity   62.0%; Pred. No. 1e-29;
Matches   75; Conservative 16; Mismatches 24; Indels   6; Gaps   1;

```
Qy  20 EVOLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY   79
        |||||||| ||||||||||:|| |||:| | |  | |||:|   | |||||  | |:|
Db   1 EVOLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY   60

Qy  80 DPKFQGKRATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYYAMDYWGQGTSVT 139
         :|||:| || | |:|||||||:|:|||||:|||:|||  |          |||:|| ||||
Db  61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-----WYFDVWGAGTTVT    114

Qy 140 V 140
         |
Db 115 V 115
```

RESULT 14

```
ID   HV01_MOUSE     STANDARD;      PRT;   121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
```

Query Match   52.8%; Score 379; DB 1; Length 117;

DR   PIR; A02027; GVMS11.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER   121   121
SQ   SEQUENCE   121 AA;   13135 MW;   227AEF3EC56ED0BF CRC64;

Query Match   50.8%;   Score 379;   DB 1;   Length 121;
Best Local Similarity   62.0%;   Pred. No. 1.1e-29;
Matches 75; Conservative 17; Mismatches 27; Indels 2; Gaps 2;

```
Qy   20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY  79
             ||||||||||| |::|| |||||||||||:|||||||||| ||:|||||
Db    1  EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY  60

Qy   80  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYGYGNYGVYYAMDVWGQGTSVT  139
             :|||||||||||:|:||||||||||||||:||||||||:|  |||||::|
Db   61  NDNLKGKATLPADTSSSTAYIQLSSLTSEDSAIYHCAR-GIYYNSSPY-FDSWGQGTTLT  118

Qy  140  V  140
            |
Db  119  V  119
```

RESULT 15
HV1C_HUMAN

ID   HV1C_HUMAN   STANDARD;   PRT;   147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC   PROTEIN.
DR   PIR; A02026; E1HUND.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   147   IG HEAVY CHAIN V-I REGION ND.
FT   MOD_RES   20   20   PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID   41   115
FT   CONFLICT   21   21   T -> V (IN REF. 2).
FT   CONFLICT   53   54   IH -> HI (IN REF. 2).
FT   CONFLICT   67   68   VG -> GV (IN REF. 2).
FT   CONFLICT 125   125   MISSING (IN REF. 2).
FT   NON_TER   147   147
SQ   SEQUENCE   147 AA;   16491 MW;   948F9F72A5366CC20 CRC64;

Query Match   50.7%;   Score 378.5;   DB 1;   Length 147;
Best Local Similarity   52.6%;   Pred. No. 1.5e-29;
Matches 72; Conservative 25; Mismatches 35; Indels 5; Gaps 1;

```
Qy    9  FLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIG  68
         ||:|      |:||||||||| |||||||:|| :||||| :||:|||| | ||:|||||
Db    9  FLVAAATRVHSQTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVG  68

Qy   69  RIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-----EGYYGN  123
          |:|  |  |   ||||:.||.||:| |||:| |.:| ||:||:|:||||     ||||:
Db   69  WINPNSGGTNYAPRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNF  128

Qy  124  YGVYAMDYWGQGTSVTV  140
          | :|| |||||||:||
Db  129  DYSYTLDVWGQGTTVTV  145
```

Search completed: May 7, 2002, 12:32:34
Job time: 565 sec

OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: May   7, 2002, 12:22:25 ; Search time 67.39 Seconds
                                               (without alignments)
                                               116.512 Million cell updates/sec

Title: us-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT..........YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
                     Gapop 10.0 , Gapext 0.5
Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   A_Geneseq_1101:*
                     Listing first 45 summaries

                     1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
                     2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
                     3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
                     4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
                     5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
                     6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
                     7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
                     8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
                     9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
                    10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
                    11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
                    12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
                    13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
                    14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
                    15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
                    16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
                    17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
                    18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
                    19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
                    20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
                    21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
                    22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	16	AAR81321	Humanized anti-VLA
2	562	100.0	106	16	AAW22412	Humanised alpha-4
3	562	100.0	126	18	AAW22419	Humanised alpha-4
4	508	90.4	106	16	AAR81328	Mouse anti-VLA-4 a
5	508	90.4	126	16	AAR81326	Mouse VLA-4 antibo
6	508	90.4	126	16	AAR81332	Human VLA-4 antibo
7	508	90.4	126	18	AAW22409	Alpha-4 integrin m
8	488	86.8	359	20	AAY29913	Humanized VLA-4 reshap
9	488	86.8	20	20	AAY29911	Human MCP-3 and mu
10	488	86.8	374	20	AAY29916	Human IP-10 and mu
11	481	85.6	128	15	AAR60627	Artificial synthet
						MEI-14 light chain

RESULT   1
AAR81321

ID   AAR81321 standard; Protein; 106 AA.
XX
AC   AAR81321;
XX
DT   02-APR-1996 (first entry)
XX
DE   Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Chimeric Mus musculus.
OS   Chimeric Homo sapiens.
XX
PN   WO951979O-Al.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
XX   inflammatory disease.

ALIGNMENTS

12	475.5	84.6	234	12	AAR13050	CD4-specific CDR-g
13	471.5	83.9	107	16	AAR78970	Light chain variab
14	465	82.7	108	17	AAR91159	Murine monoclonal
15	460.5	81.9	128	11	AAR06252	Variable region of
16	460	81.9	637	13	AAR26983	(FRP51)-ETA fusion
17	456	81.1	109	19	AAW26797	Anti-gp54 MAb T16
18	455	81.0	240	16	AAW85495	ScFv(FRP51). Synt
19	455	81.0	241	20	AAY21882	Amino acid sequenc
20	455	81.0	245	19	AAW26800	Anti-gp54 MAb T16
21	453.5	80.7	107	16	AAR81322	Humanized VLA-4 an
22	453.5	80.7	107	18	AAR81322	Humanized alpha-4
23	453	80.6	109	12	AAR13658	Murine OKT4A light
24	452	80.4	241	13	AAR26981	FRP51 fusion prote
25	451.5	80.3	241	16	AAR65163	Human REI monoclon
26	451.5	80.3	129	15	AAR47207	Human/murine IL-1
27	451	80.2	355	18	AAW35133	R. pipiens recombi
28	450	80.0	107	19	AAW86805	Variable light dom
29	449.5	79.9	107	18	AAW70625	Humanised murine a
30	449.5	79.9	107	19	AAW10231	CDR-grafted light
31	446.5	79.4	110	19	AAW70673	Anti-VEGF humanise
32	446.5	79.4	234	18	AAW10233	TF8-5G9 CDR-grafte
33	446.5	79.4	237	19	AAW70703	Protein encoded by
34	445.5	79.3	107	19	AAW86804	Variable light dom
35	445.5	79.3	107	19	AAW70623	Humanised murine a
36	445	79.1	107	20	AAW87455	Humanised anti-alp
37	444.5	79.1	107	22	AAB62087	Human V1 consensus
38	444.5	79.1	107	22	AAB60400	Consensus human li
39	444.5	79.1	107	22	AAB61585	Human variable lig
40	444.5	79.1	108	19	AAW70622	Human consensus fr
41	444.5	79.1	108	21	AAY82345	Human consensus se
42	444.5	79.1	126	13	AAR29015	pUC-RV1-PMla. Syn
43	444.5	79.1	126	13	AAR29013	pUC-RVh-PMla. Syn
44	444.5	79.1	256	21	AAY55072	Interleukin-6 spec
45	444.5	79.1	260	21	AAY55075	Single chain Fv pr

PS   Claim 9; Page 67; 105pp; English.
XX
CC   The sequence encodes the humanized mouse antibody 21.6 light chain
CC   variable region, La, directed against leukocyte adhesion molecule
CC   VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC   AAQ99892) regions are linked to human constant regions in the
CC   construction of a humanized antibody against VLA-4. The 5' and 3'
CC   ends of the mouse cDNAs are modified using PCR primers (See
CC   AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC   containing human kappa or gamma-1 constant regions. In the humanized
CC   light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC   VR framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
CC   antibodies are transfected into COS cells. The humanized antibodies
CC   can be used for inhibiting adhesion of a leukocyte to an endothelial
CC   cell and for treating inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;

Query Match   100.0%;   Score 562;   DB 16;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 6.9e-37;
Matches 106; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMANYQQTPGKAPRLLIHTSALQPGIPS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprlllhytsalqpgips 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYCLCLQYDNLWTFGQGTKVEIK 106
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106

FT   CDR2 loop"
FT   Region   50..56
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   Region   57..88
FT   /label= FR3
FT   /note= "REI framework region 3"
FT   Misc-difference 58
FT   /note= "REI Val-58 is substd. by Ile of mouse
FT   21.6 VL, important in supporting the CDR2
FT   loop"
FT   Misc-difference 69
FT   /note= "REI Thr-69 is substd. by Arg of mouse
FT   21.6 VL, involved in antibody-antigen
FT   binding"
FT   Region   89..96
FT   /label= CDR3
FT   /note= "21.6 complementarity determining region 3"
FT   Region   97..106
FT   /label= FR4
FT   /note= "REI framework region 4"
FT   Misc-difference 103
FT   /note= "REI Leu-103 substd. by Val, more typical
FT   of human kappa light chain J region"
FT   Misc-difference 104
FT   /note= "REI Gln-104 substd. by Glu, more typical
FT   of human kappa light chain J region"
FT   Misc-difference 106
FT   /note= "REI Thr-106 substd. by Lys, more typical
FT   of human kappa light chain J region"
XX

CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework. It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
XX
SQ   Sequence   106 AA;

RESULT 3

```
Query Match             100.0%;  Score 562;  DB 18;  Length 126;
Best Local Similarity   100.0%;  Pred. No. 8.1e-37;
Matches 106;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprlllihytsalqpgips 80

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
       ||||||||||||||||||||||||||||||||||||||||||||||
Db 81 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 126
```

AAW22419

```
ID   AAW22419 standard; Protein; 126 AA.
XX
AC   AAW22419;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key          Location/Qualifiers
FH
FT   Peptide       1..20
FT                /label= Leader
FT   Protein       21..126
FT                /label= Mat_protein
FT                /note= "VL version La (Claim 25)"
FT   Region        21..43
FT                /label= FR1
FT                /note= "REI framework region 1"
FT   Region        44..54
FT                /label= CDR1
FT                /note= "21.6 complementarity determining region 1"
FT   Region        55..69
FT                /label= FR2
FT                /note= "REI framework region 2"
FT   Region        70..76
FT                /label= CDR2
FT                /note= "21.6 complementarity determining region 2"
FT   Region        77..108
FT                /label= FR3
FT                /note= "REI framework region 3"
FT   Region        109..116
FT                /label= CDR3
FT                /note= "21.6 complementarity determining region 3"
FT   Region        117..126
FT                /label= FR4
FT                /note= "REI framework region 4"
XX
PN   WO9718838-A1.
PD   29-MAY-1997.
PF   21-NOV-1996;  96WO-US18807.
PR   21-NOV-1995;  95US-0561521.
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74788.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 10; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22412).  It is composed of complementarity determining regions from
CC   the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human REI framework.  It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences.  The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence  126 AA;
```

RESULT 4

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Query Match             100.0%;  Score 562;  DB 18;  Length 106;
Best Local Similarity   100.0%;  Pred. No. 6.9e-37;
Matches 106;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprlllihytsalqpgips 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
       ||||||||||||||||||||||||||||||||||||||||||||||
Db 61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106
```

AAR81328

```
ID   AAR81328 standard; Protein; 106 AA.
XX
AC   AAR81328;
XX
DT   02-APR-1996 (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key          Location/Qualifiers
FH
FT   Region        1..23
FT                /label= FR1
FT                /note= "mouse light chain variable framework
FT                region 1"
FT   Region        24..34
FT                /label= CDR1
FT                /note= "mouse light chain variable complementarity
FT                determining region 1"
FT   Region        35..49
FT                /label= FR2
FT                /note= "mouse light chain variable framework
FT                region 2"
FT   Region        50..56
FT                /label= CDR2
```

```
RESULT 5
AAR81326
ID   AAR81326 standard; Protein; 126 AA.

Query Match             94;
Best Local Similarity   90.4%;
                        Score 508; DB 16; Length 106;
                        88.7%;   Pred. No. 1.1e-32;
Matches   94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||:|:|:|||||||||:|||||||||:|||||:||||||||||||||||||
Db    1  diqmtqspsslsasggkvtitcktsqdinkymawyqhkpgkrpllihytsalqpgips   60

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||||:|:||:||||||||||||||||||||||| |||:|||
Db   61  rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 106
```

```
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "mouse light chain variable complementarity
FT                   determining region 2"
FT   Region          89..96
FT                   /label= CDR3
FT                   /note= "mouse light chain variable framework
FT                   region 3"
FT   Region          97..106
FT                   /label= FR4
FT                   /note= "mouse light chain variable complementarity
FT                   determining region 3"
FT                   /note= "mouse light chain variable framework
FT                   region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 66; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ9895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;
```

```
XX
AC   AAR81326;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99889.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 1; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 light chain variable
CC   region directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (see AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;
```

```
Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||:| ||||||||||||||||| |||||||||||||||||||||
Db   21 diqmtqspsslsasiggkvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        |||||||||:||:|:||||||||||||||||||||||  |||:|||
Db   81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126
```

```
Query Match     90.4%;     Score 508;  DB 16;    Length 126;
Best Local Similarity  88.7%;     Pred. No. 1.2e-32;
Matches  94;  Conservative  6;  Mismatches  6;  Indels  0;  Gaps  0;
```

RESULT 6
AAR81332
```
ID   AAR81332 standard; Protein; 126 AA.
XX
AC   AAR81332;
XX
DT   23-MAR-1996 (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key         Location/Qualifiers
FH
FT   Peptide     1..20
FT               /note= "signal peptide"
FT   Region      21..43
FT               /note= "framework region 1"
FT   Region      44..54
FT               /note= "complementarity determining region 1"
FT   Region      55..69
FT               /note= "framework region 2"
FT   Region      70..76
FT               /note= "complementarity determining region 2"
FT   Region      77..108
FT               /note= "framework region 3"
FT   Region      109..116
FT               /note= "complementarity determining region 3"
FT   Region      117..126
FT               /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99893.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 10; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 light
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
CC   then subcloned into mammalian cell expression vectors containing
CC   human kappa or gamma-1 constant regions. In the humanized light
CC   chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells. The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis. They can also be used in the treatment of
CC   stroke, cerebral traumas, meningitis or encephalitis. The
CC   antibodies can also be used for detecting VLA-4, for affinity
CC   purification or for generating anti-idiotype antibodies.
XX
SQ   Sequence  126 AA;
```

```
Query Match     90.4%;     Score 508;  DB 16;    Length 126;
Best Local Similarity  88.7%;     Pred. No. 1.2e-32;
Matches  94;  Conservative  6;  Mismatches  6;  Indels  0;  Gaps  0;
```

```
Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||:| ||||||||||||||||| |||||||||||||||||||||
Db   21 diqmtqspsslsasiggkvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        |||||||||:||:|:||||||||||||||||||||||  |||:|||
Db   81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126
```

RESULT 7
AAW22409
```
ID   AAW22409 standard; Protein; 126 AA.
XX
AC   AAW22409;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VL region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key         Location/Qualifiers
FH
FT   Peptide     1..20
FT               /label= Leader
FT   Region      21..43
FT               /label= FR1
FT               /note= "framework region 1"
FT   Region      44..54
FT               /label= CDR1
FT               /note= "complementarity determining region 1"
FT   Region      55..69
FT               /label= FR2
FT               /note= "framework region 2"
FT   Region      70..76
FT               /label= CDR2
FT               /note= "complementarity determining region 2"
FT   Region      77..108
FT               /label= FR3
FT               /note= "framework region 3"
FT   Region      109..116
FT               /label= CDR3
FT               /note= "complementarity determining region 3"
FT   Region      117..126
FT               /label= FR4
FT               /note= "framework region 4"
```

PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996; 96WO-US18807.
XX
PR   21-NOV-1995; 95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74759.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 68; 107pp; English.
XX
CC   This polypeptide comprises the light chain variable region (VL) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC   complementarity determining regions (CDRs) of the 21.6 VL can be
CC   incorporated into a human REI framework to produce a claimed
CC   humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;

Query Match   90.4%; Score 508; DB 18; Length 126;
Best Local Similarity   88.7%;
  Matches   94; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

```
Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              ||||||||||||||| |||||||||:|||||||||||| |:||||||||||||||||||||
Db         21 diqmtqspsslsaslggkvtitcksqdinkymawyqhkpgkrprllihytsalqpgips 80

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
              ||||||||||||:|:|||||||||||||||||||||| |||:|||||
Db         81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126
```

RESULT 8
AAY29913

ID   AAY29913 standard; Protein; 359 AA.
XX
AC   AAY29913;
XX
DT   17-NOV-1999 (first entry)
XX
DE   Human MCP-3 and murine scFv38 fusion protein.
XX
KW   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW   immune response; HIV; infection.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
XX
PN   WO9946392-A1.
XX
PD   16-SEP-1999.

XX
PF   12-MAR-1999; 99WO-US05345.
XX
PR   12-MAR-1998; 98US-0077745.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kwak LW, Biragyn A;
XX
DR   WPI; 1999-551418/46.
XX
PT   New fusion polypeptides comprising a chemokine and a tumour antigen or
PT   HIV antigen, used for treating cancers or treating or preventing HIV
PT   infection
XX
PS   Disclosure; Page 118-119; 142pp; English.
XX
CC   The present invention describes fusion proteins comprising a chemokine
CC   and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC   comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC   Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC   (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC   SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC   HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC   gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC   be used for producing an immune response, e.g. an effector T cell immune
CC   response. They can also be used for treating cancer or treating or
CC   preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC   can be used in in vitro diagnostic assays, as well as in screening assays
CC   for identifying unknown tumour antigen epitopes and fine mapping of
CC   tumour antigen epitopes. The present sequence represents a fusion protein
CC   from the present invention.
XX
SQ   Sequence   359 AA;

Query Match   86.8%; Score 488; DB 20; Length 359;
Best Local Similarity   84.9%;
  Matches   90; Conservative   9; Mismatches   7; Indels   0; Gaps   0;

```
Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||||||||||||| ||||||||:|||||||||||| ||| ||:||||||||| ||||||
Db        233 diqmtqspsslsaslggkvtitckasqdinkyjawyqhkpgksprllihytstlqpgips 292

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
              |||||||||||:|:|||||||||||||||||:| |||||:|||||
Db        293 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 338
```

RESULT 9
AAY29911

ID   AAY29911 standard; Protein; 361 AA.
XX
AC   AAY29911;
XX
DT   17-NOV-1999 (first entry)
XX
DE   Human IP-10 and murine scFv38 fusion protein.
XX
KW   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW   immune response; HIV; infection.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
XX
PN   WO9946392-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999; 99WO-US05345.
XX
PR   12-MAR-1998; 98US-0077745.

RESULT 10

```
AAY29916
ID   AAY29916 standard; Protein; 374 AA.
XX
AC   AAY29916;
XX
DT   17-NOV-1999  (first entry)
XX
DE   Artificial synthetic construct protein SEQ ID NO:15.
XX
KW   Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW   immune response; HIV; infection.
XX
OS   Synthetic.
XX
PN   WO9946392-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999;  99WO-US05345.
XX
PR   12-MAR-1998;  98US-0077745.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kwak LW, Biragyn A;
XX
DR   WPI; 1999-551418/46.
XX
PT   New fusion polypeptides comprising a chemokine and a tumour antigen or
PT   HIV antigen, used for treating cancers or treating or preventing HIV
PT   infection -
XX
PS   Disclosure; Page 115-116; 142pp; English.
XX
CC   The present invention describes fusion proteins comprising a chemokine
CC   and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC   comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC   Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC   (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC   SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC   HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC   gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC   be used for producing an immune response, e.g. an effector T cell immune
CC   response. They can also be used for treating cancer or treating or
CC   preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC   can be used in in vitro diagnostic assays, as well as in screening assays
CC   for identifying unknown tumour antigen epitopes. The present sequence
CC   represents a fusion protein
CC   from the present invention.
XX
SQ   Sequence  361 AA;

Query Match             86.8%;  Score 488;  DB 20;  Length 361;
Best Local Similarity   84.9%;  Pred. No. 1.1e-30;
Matches   90;  Conservative   9;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
         ||||||||||||||||:||:||||| ||||||||||||| |||||:|||||||||||||||
Db  235  diqmtqspsslsasiggkvtitckasqdinkyiawyqhkpgkgprllihytstlqppips  294

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK  106
         |||||||||||:|:||||||||||||:|||||||||||||:|:|||
Db  295  rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik  340
```

RESULT 11

```
AAR60627
ID   AAR60627 standard; Protein; 128 AA.
XX
AC   AAR60627;
XX
DT   04-JUN-1995  (first entry)
XX
DE   ME1-14 light chain variable region.
XX
KW   Monoclonal antibody; tumour.
XX
OS   Homo sapiens.
XX
PN   WO9421294-A.
XX
PD   29-SEP-1994.
XX
PF   14-MAR-1994;  94WO-US02724.
XX
PR   19-MAR-1993;  93US-0033864.
XX
PA   (BIGN/) BIGNER D D.
PA   (CARR/) CARREL S.
PA   (ZALU/) ZALUTSKY M R.
XX
PI   Bigner DD, Carrel S, Zalutsky MR;
XX
DR   WPI; 1994-316669/39.
DR   N-PSDB; AAQ73537.
XX
PT   Method of treating solid or cystic tumours with antibodies - by
PT   administering monoclonal antibody Me1-14, having Fc deleted,
XX
PT   New fusion polypeptides comprising a chemokine and a tumour antigen or
PT   HIV antigen, used for treating cancers or treating or preventing HIV
PT   infection -
XX
PS   Disclosure; Page 117-118; 142pp; English.
XX
CC   The present invention describes fusion proteins comprising a chemokine
CC   and a tumour antigen or HIV antigen. Specifically claimed fusion
CC   proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC   human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC   Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC   human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC   MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC   HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC   can be used for producing an immune response, e.g. an effector T cell
CC   immune response. They can also be used for treating cancer or treating
CC   or preventing HIV infection. The fusion proteins and/or nucleotide
CC   sequences can be used in in vitro diagnostic assays, as well as in
CC   screening assays for identifying unknown tumour antigen epitopes and fine
CC   mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AA221168 are
CC   sequences given in the SEQ ID LISTING in the present invention but which
CC   are not mentioned further within the specification.
XX
SQ   Sequence  374 AA;

Query Match             86.8%;  Score 488;  DB 20;  Length 374;
Best Local Similarity   84.9%;  Pred. No. 1.2e-30;
Matches   90;  Conservative   9;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
         ||||||||||||||||:||:||||| ||||||||||||| |||||:|||||||||||||||
Db   95  diqmtqspsslsasiggkvtitckasqdinkyiawyqhkpgkgprllihytstlqppips  154

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK  106
         |||||||||||:|:||||||||||||:|||||||||||||:|:|||
Db  155  rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik  200
```

PT using injection or deposition in the cyst cavity
XX
PS Disclosure; Fig 2; 31pp; English.
XX
PT
CC The sequence is that of the ME1-14 light chain. The protein is a
CC monoclonal antibody which can be administered to treat solid or
CC cystic tumours.
CC See also AAR60626.
XX
SQ Sequence 128 AA;

Query Match
Best Local Similarity 85.6%; Score 481; DB 15; Length 128;
Matches 89; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
    |||||||||||||||:|:||||||||:|:|||||||:|||||| ||||||:|||||||
Db 21 diqmtqspsslsaslggkvtitckasqdinkylawyqhkpgkgprllmhytstlqpgvps 80

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
    |||||||||||:|:|:||:|||||||||||||||:|||||||||:||
Db 81 rfsgsgsgrdysfsisnlepediatyyclqydnlltfgggtkleik 126

RESULT 12
AAR13050
ID AAR13050 standard; Protein; 234 AA.
XX
AC AAR13050;
XX
DT 27-SEP-1991 (first entry)
XX
DE CD4-specific CDR-grafted light chain.
KW variable region; antibody; OKT4A; heavy chain; CD4;
KW complementary determining region.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal sequence
FT Region 21..45
FT /label= framework region 1
FT Region 46..52
FT /label= CDR 1
FT Region 53..69
FT /label= framework region 2
FT Region 70..76
FT /label= CDR 2
FT Region 77..110
FT /label= framework region 3
FT Region 111..116
FT /label= CDR 3
FT Region 117..132
FT /label= framework region 4
FT Region 133..234
FT /label= kappa constant domain

PN WO9109966-A.
XX
PD 11-JUL-1991.
XX
PF 21-DEC-1990; 90WO-GB02015.
XX
PR 21-DEC-1989; 89GB-0028874.
PR 21-DEC-1990; 90WO-GB02017.
PR 21-DEC-1990; 90WO-GB02018.
XX
PA (ORTH) ORTHO PHARM CORP.
XX
PI Jolliffe LK, Zivin RA, Pulito VL, Adair JR, Athwal DS;

XX
DR WPI; 1991-222914/30.
DR N-PSDB; AAQ12633.
XX
PT
PT New CD4 specific recombinant - complementarity determining region
PT grafted antibody for treating graft rejection and T cell
PT disorders
XX
PS Claim 1; Fig 8; 96pp; English.
XX
CC This is an example of a CDR-grafted light chain of the invention.
CC The constant regions are based on sequences of the human kappa
CC constant domain, the signal sequence is derived from murine MAb
CC B72.3 and the CDR sequences are based on the murine OKT4A light chain
CC CDRs. The recombinant antibody encoded by this sequence has affinity
CC for CD4 similar to that of OKT4A.
CC See also AAQ12627-Q12632.
XX
SQ Sequence 234 AA;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
    |||||||||||||||||||||||||| ||| |:| |||||||||||||:|||:|||:|:||
Db 21 diqmtqspsslsasvgdrvtitckaspdinkylnwyqqtpgkapkllilyytstlqpgvps 80

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
    |||||||| :|||||||||||||||||||| ||| |:||||||||:|
Db 81 rfsgsgsgteyftftisslqpediatyycqaydnllfffgggtkiqi 126

RESULT 13
AAR78970
ID AAR78970 standard; Protein; 107 AA.
XX
AC AAR78970;
XX
DT 21-DEC-1995 (first entry)
XX
DE Light chain variable region for monoclonal antibody 23F8.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW light chain.
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
DR WPI; 1995-275415/36.
DR N-PSDB; AAQ97508.
XX
PT
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX
PS Claim 23; Page 67-68; 106pp; English.
XX
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate

Query Match
Best Local Similarity 84.6%; Score 475.5; DB 12; Length 234;
Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

```
CC   covalent compound which was covalently bound to keyhole limpet
CC   hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC   5B6 and 3E8) were producing MAbs that were strongly positive
CC   against glutathione-mercuric ions but negative against glutathione
CC   without mercuric ions. RNA was isolated from hybridoma cells with
CC   guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC   by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC   were complementary to the 5' end of the CH1 domain of the heavy
CC   chain expressed by the hybridoma of interest, or to the 5' and of
CC   the C kappa domain. Some of the primers used for cDNA synthesis are
CC   shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate V-region primer. In addition, the VH primer AAQ97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in AAQ97499-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC   AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
XX
SQ   Sequence   107 AA;
```

```
RESULT 14
AAR93159
ID   AAR93159 standard; protein; 108 AA.
XX
AC   AAR93159;
XX
DT   24-OCT-1996 (first entry)
XX
DE   Murine monoclonal antibody K20 kappa chain variable region.
XX
KW   Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW   beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW   T cell activation; complementary determining region; CDR.
XX
OS   Mus musculus.
```

```
FH   Key              Location/Qualifiers
FH
FT   Region           1..23
FT                    /label= FR1
FT                    /note= "framework region"
FT   Region           24..34
FT                    /label= CDR1
FT                    /note= "complementary determining region"
FT   Region           35..49
FT                    /label= FR2
FT                    /note= "framework region"
FT   Region           50..56
FT                    /label= CDR2
FT                    /note= "complementary determining region"
FT   Region           57..88
FT                    /label= FR3
FT                    /note= "framework region"
FT   Region           89..94
FT                    /label= CDR3
FT                    /note= "complementary determining region"
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Query Match      83.9%;  Score 471.5;  DB 16;  Length 107;
Best Local Similarity   83.2%;       Pred. No. 7.2e-30;
Matches   89; Conservative   9; Mismatches   8; Indels   1; Gaps   1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||||||:||||:||||||:|||||: :|||||||||:||||||||||:|||  ||||:|||
Db          1 diqmtqspsslsasiggkvtitckasqdinkyiawyqhkpgkqprllihytstlqpgips 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
              ||||||||||||:|:|||||||||||||||||| :|||||||||:|||
Db         61 rfsgsgsgrdysfsisnpediatyyclqydnsiftfgsgtkleik 107
```

```
RESULT 15
AAR06252
ID   AAR06252 standard; protein; 128 AA.
XX
AC   AAR06252;
XX
DT   10-DEC-1990 (first entry)
XX
DE   Variable region of murine AHT 107 light chain.
XX
KW   Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
XX
OS   Mus sp.
XX
PN   EP380068-A.
XX
PD   01-AUG-1990.
XX
PF   24-JAN-1990;   90EP-0101351.
XX
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Query Match      82.7%;  Score 465;  DB 17;  Length 108;
Best Local Similarity   81.1%;       Pred. No. 2.3e-29;
Matches   86; Conservative   10; Mismatches   10; Indels   0; Gaps   0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              ||:|||||||||||||||:||||:|||||||||||||:|||||:|||||||||:||||||
Db          1 diqltqspslsasiggkvtitckasqdinkyiawyqhqhepgkgprllirytsklesgips 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
              |||||||||||:|:||||||||||| ||||||| |||:||||||||
Db         61 rfsgsgsgrdysfsisnlepediatyyclqgyynlwtfgggtkleik 106
```

```
CC   The present sequence is that of the variable region of the kappa
CC   light chain from murine monoclonal antibody K20. The antibody
CC   recognises the beta 1 subunit (CD29) of integrins and inhibits
CC   activation and proliferation of peripheral T cells induced by
CC   anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC   for humanisation; the humanised version may be useful as an
CC   immunosuppressant. In the humanisation process, the complementarity
CC   determining regions (CDRs) of a human antibody with framework
CC   regions 70-95% homologous to those of K20 were replaced by the K20
CC   CDRs.
XX
SQ   Sequence   108 AA;
```

```
PS   Example 1; Fig 2A; 39pp; French.
XX
XX
DR   WPI; 1996-162083/17.
DR   N-PSDB; AAT26849.
XX
CC   Humanisation of non-human immunoglobulin variable regions - for
CC   prodn. of humanised antibodies, esp. K20, e.g. as an
CC   immunosuppressant
XX
PT   FR2724393-A1.
XX
PI   Bernard A,  Cervoni MF,  Lefranc MP,  Margaritte C;
PI   Poul MA;
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (PROT-) PROTEINE PERFORMANCE SA.
XX
PR   12-SEP-1994;   94FR-0010858.
XX
PF   12-SEP-1994;   94FR-0010858.
XX
PD   15-MAR-1996.
XX
PN   FR2724393-A1.
XX
FT   Region           95..108
FT                    /label= J_kappa1
```

PR   04-DEC-1989;   89US-0441702.
PR   24-JAN-1989;   89US-0301216.
XX
PA   (MOLE-) MOLECULAR THERAPEU.
XX
PI   Zerler B;
XX
DR   WPI; 1990-232892/31.
DR   N-PSDB; AAO05556.
XX
PS   Disclosure; ; p; English.
XX
PT   Expression vectors for producing chimeric monoclonal antibodies -
PT   which express human constant region and non-human variable region
XX
CC   MAbs comprising mouse CH and CL constant regions whith human
CC   variable regions may be used to create mouse/human hybrid MAbs,
CC   which have a longer serum half-life. Method can be used to produce
CC   Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ   Sequence   128 AA;

Query Match   81.9%;   Score 460.5;   DB 11;   Length 128;
Best Local Similarity   76.6%;   Pred. No. 6e-29;
Matches   82; Conservative 18; Mismatches   6;   Indels   1; Gaps   1;

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          ||||||||||||||:|||:|:||||||||||||||||||:||:::|||||:|||||||||
Db   21 diqmtqspsslsaslggkvtltcktsqdinkfiawyqhkpgepprliihytstlqpgips 80

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFCGGTKVEIK 106
          |||||||||:||:||:::||||||||||||||||| |||| |||:|::
Db   81 rfsgsgsgkdysfsinnlepediatyyclryddlpwtfgggtklevr 127

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:04 ; Search time 32.41 Seconds
                 (without alignments)
                 73.599 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	2	US-08-561-521-7	Sequence 7, Appli
2	562	100.0	106	2	PCT-US95-01219-7	Sequence 7, Appli
3	508	90.4	106	2	US-08-561-521-5	Sequence 5, Appli
4	508	90.4	106	5	PCT-US95-01219-5	Sequence 5, Appli
5	508	90.4	126	2	US-08-561-521-2	Sequence 2, Appli
6	508	90.4	126	5	PCT-US95-01219-2	Sequence 2, Appli
7	508	90.4	126	5	PCT-US95-01219-15	Sequence 15, Appli
8	508	90.4	126	2	US-08-339-582-4	Sequence 4, Appli
9	481	85.6	128	1	PCT-US95-01219-15	Sequence 15, Appli
10	471.5	83.9	107	2	US-08-888-366-22	Sequence 22, Appl
11	460	81.9	637	2	US-08-235-838-16	Sequence 16, Appl
12	460	81.9	637	2	US-08-465-473B-16	Sequence 16, Appl
13	455	81.0	241	1	US-08-235-838-11	Sequence 11, Appl
14	455	81.0	241	2	US-08-465-473B-11	Sequence 11, Appl
15	454.5	80.9	108	2	US-08-602-725-29	Sequence 29, Appl
16	453.5	80.7	107	5	US-08-561-521-8	Sequence 8, Appli
17	453.5	80.7	107	2	PCT-US95-01219-8	Sequence 8, Appl
18	451	80.2	355	3	US-08-875-811-57	Sequence 57, Appl
19	448.5	79.8	107	3	US-07-934-373C-17	Sequence 17, Appl
20	448.5	79.8	107	5	PCT-US93-07832-17	Sequence 17, Appl
21	448.5	79.8	107	3	US-08-437-642B-17	Sequence 17, Appl
22	444.5	79.1	107	3	US-07-934-373C-18	Sequence 18, Appl
23	444.5	79.1	107	3	US-08-437-642B-18	Sequence 18, Appl
24	444.5	79.1	107	5	PCT-US93-07832-18	Sequence 18, Appl
25	444.5	79.1	108	3	US-08-974-899-3	Sequence 3, Appl
26	444.5	79.1	111	2	US-08-137-117D-67	Sequence 67, Appl
27	444.5	79.1	111	2	US-08-436-717-67	Sequence 67, Appl
28	444.5	79.1	126	1	US-08-137-117D-71	Sequence 71, Appl
29	444.5	79.1	126	2	US-08-436-717-71	Sequence 71, Appl
30	443.5	78.9	107	2	US-08-561-521-6	Sequence 6, Appli
31	443.5	78.9	107	2	US-08-652-558-34	Sequence 34, Appl
32	443.5	78.9	107	5	PCT-US95-01219-6	Sequence 6, Appli
33	443.5	78.9	108	5	PCT-US95-01219-6	Sequence 6, Appli
34	441.5	78.6	107	2	US-08-070-116A-7	Sequence 7, Appli
35	441.5	78.6	107	2	US-08-318-157B-6	Sequence 6, Appli
36	440.5	78.4	107	2	US-08-318-157B-9	Sequence 9, Appli
37	440.5	78.4	109	2	US-08-652-558-2	Sequence 2, Appli
38	440.5	78.4	109	5	PCT-US93-07832-3	Sequence 3, Appli
39	440.5	78.4	109	5	US-07-934-373C-3	Sequence 3, Appli
40	440.5	78.4	214	5	PCT-US93-07832-39	Sequence 39, Appl
41	440.5	78.4	214	5	US-07-934-373C-39	Sequence 39, Appl
42	440.5	78.4	214	3	US-08-437-642B-39	Sequence 39, Appl
43	438.5	78.0	107	4	US-07-934-373C-47	Sequence 47, Appl
44	438.5	78.0	109	2	US-09-254-189-1	Sequence 47, Appl
45	438.5	78.0	109	3	US-08-437-642B-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-561-521-7

Query Match   100.0%; Score 562; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1e-45;

2

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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RESULT 2
PCT-US95-01219-7
Sequence 7, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 100.0%; Score 562; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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RESULT 3
US-08-561-521-5

Sequence 5, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-5

Query Match 90.4%; Score 508; DB 2; Length 106;
Best Local Similarity 88.7%; Pred. No. 1.1e-40;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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       |||||||||||:|| ||||||||||||||||||||| |||||||||||||||||||||
Db  1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGGGTKVEIK 106
        ||||||||||:||:|:||||||||||||||||||||| ||:|||
Db 61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
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RESULT 4
PCT-US95-01219-5
Sequence 5, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
PCT-US95-01219-5
MOLECULE TYPE: protein
TOPOLOGY: linear
STRANDEDNESS: single
TYPE: amino acid
LENGTH: 106 amino acids
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 5:

Query Match   90.4%;   Score 508;   DB 5;   Length 106;
Best Local Similarity   88.7%;   Pred. No. 1.1e-40;
Matches   94;   Conservative   6;   Mismatches   6;   Indels   0;   Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||:|:||||||||||||||||| ||||||||||||||||||||||||
Db 1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||||||:|:|:||||||||||||||||||||||| ||:|||
Db 61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106

RESULT 5
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-2

Query Match   90.4%;   Score 508;   DB 2;   Length 126;
Best Local Similarity   88.7%;   Pred. No. 1.3e-40;
Matches   94;   Conservative   6;   Mismatches   6;   Indels   0;   Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||:|:||||||||||||||||| ||||||||||||||||||||||||
Db 21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy 61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||||||:|:|:||||||||||||||||||||||| ||:|||
Db 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126

RESULT 6
US-08-561-521-15
; Sequence 15, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:

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;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-15
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Query Match         90.4%;   Score 508;  DB 2;   Length 126;
Best Local Similarity    88.7%;   Pred. No. 1.3e-40;
Matches 94;   Conservative  6;   Mismatches  6;   Indels  0;   Gaps  0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSODINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||:| ||||||||||||||||||||||||||:||
Db  21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||||:| ||:|:|||||||||||||||||| ||:|||
Db  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
```

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RESULT 7
PCT-US95-01219-2
;   Sequence 2, Application PC/TUS9501219
;   GENERAL INFORMATION:
;       APPLICANT: Bendig, Mary M.
;       APPLICANT: Leger, Olivier J.
;       APPLICANT: Saldanha, Jose
;       APPLICANT: Jones, S. Tarran
;       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;       TITLE OF INVENTION: Adhesion Molecule VLA-4
;       NUMBER OF SEQUENCES: 45
;       CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend Khourie and Crew
;       STREET: One Market Plaza, Steuart Tower, Suite 2000
;       CITY: San Francisco
;       STATE: California
;       COUNTRY: USA
;       ZIP: 94105
;       COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US 08/186,269
;       FILING DATE: 25-JAN-1994
;       CLASSIFICATION:
;       PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: PCT/US95/01219
;       FILING DATE: 25-JAN-1995
;       CLASSIFICATION:
;       ATTORNEY/AGENT INFORMATION:
;       NAME: Smith, William L.
;       REGISTRATION NUMBER: 30,223
;       REFERENCE/DOCKET NUMBER: 15270-14
;       TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 415-543-9600
;       TELEFAX: 415-543-5043
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 126 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
PCT-US95-01219-2
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RESULT 8
PCT-US95-01219-15
;   Sequence 15, Application PC/TUS9501219
;   GENERAL INFORMATION:
;       APPLICANT: Bendig, Mary M.
;       APPLICANT: Leger, Olivier J.
;       APPLICANT: Saldanha, Jose
;       APPLICANT: Jones, S. Tarran
;       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;       TITLE OF INVENTION: Adhesion Molecule VLA-4
;       NUMBER OF SEQUENCES: 45
;       CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend Khourie and Crew
;       STREET: One Market Plaza, Steuart Tower, Suite 2000
;       CITY: San Francisco
;       STATE: California
;       COUNTRY: USA
;       ZIP: 94105
;       COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US 08/186,269
;       FILING DATE: 25-JAN-1994
;       CLASSIFICATION:
;       PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: PCT/US95/01219
;       FILING DATE: 25-JAN-1995
;       CLASSIFICATION:
;       ATTORNEY/AGENT INFORMATION:
;       NAME: Smith, William L.
;       REGISTRATION NUMBER: 30,223
;       REFERENCE/DOCKET NUMBER: 15270-14
;       TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 415-543-9600
;       TELEFAX: 415-543-5043
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 126 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
PCT-US95-01219-15
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Query Match         90.4%;   Score 508;  DB 5;   Length 126;
Best Local Similarity    88.7%;   Pred. No. 1.3e-40;
Matches 94;   Conservative  6;   Mismatches  6;   Indels  0;   Gaps  0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSODINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||:| ||||||||||||||||||||||||||:||
Db  21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||||:| ||:|:|||||||||||||||||| ||:|||
Db  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
```

```
Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
         |||||||||:| ||:|:|||||||||||||||||| ||:|||
Db  81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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RESULT 9
US-08-339-582-4
;   Sequence 4, Application US/08339582
;   Patent No. 5558852
;   GENERAL INFORMATION:
;       APPLICANT: Bigner, Darell D.
;       APPLICANT: Zalutsky, Michael R.
;       APPLICANT: Carrel, Stefan
```

TITLE OF INVENTION: METHOD OF TREATMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,582
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3175
TELEFAX: 919-420-2200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-582-4

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Query Match          85.6%;  Score 481;  DB 1;  Length 128;
Best Local Similarity  84.0%;  Pred. No. 4.3e-38;
Matches    89;  Conservative  9;  Mismatches  8;  Indels  0;  Gaps  0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||||||:|:||||||||||||:|||||||||||||||||:|:|||
Db  21 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        ||||||||||:|:|||:|:||||||||||||||| ||||||:||||
Db  81 RFSGSGSGRDYSFSISNLEPEDIATYCLQYDNLLTFGGGTKLEIK 126
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RESULT 10
US-08-888-366-22
Sequence 22, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.395USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-366-22

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Query Match          83.9%;  Score 471.5;  DB 2;  Length 107;
Best Local Similarity  83.2%;  Pred. No. 2.7e-37;
Matches    89;  Conservative  9;  Mismatches  8;  Indels  1;  Gaps  1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||||||:|:||||||||||||:|||||||||||||||||:|:|||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
        ||||||||||:|:|||:|:|||||||||||||| |:|||||||:||||
Db  61 RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGGGTKLEIK 107
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RESULT 11
US-08-235-838-16
Sequence 16, Application US/08235838
Patent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA

RESULT 12
US-08-465-473B-16
Sequence 16, Application US/0845473B
Patent No. 5939531
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 593953lman
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
CLASSIFICATION: 435
FILING DATE: 5 June 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-838-16

Query Match   81.9%; Score 460; DB 1; Length 637;
Best Local Similarity 80.2%; Pred. No. 2.3e-35;
Matches   85; Conservative   10; Mismatches   11; Indels   0; Gaps   0;

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Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||| |||||||||| ||  |||||||:||||| | |||||  ||||||||||| |||||||
Db  168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        |||||||||||:|:|| ||:||||||||| |||  |||||||:||||
Db  228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYLTFGGGTKLEIK 273
```

RESULT 13
US-08-235-838-11
Sequence 11, Application US/0823583B
Patent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6955
TELEFAX: (908)522 6940
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-473B-16

Query Match   81.9%; Score 460; DB 2; Length 637;
Best Local Similarity 80.2%; Pred. No. 2.3e-35;
Matches   85; Conservative   10; Mismatches   11; Indels   0; Gaps   0;

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Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||| |||||||||| ||  |||||||:||||| | |||||  ||||||||||| |||||||
Db  168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        |||||||||||:|:|| ||:||||||||| |||  |||||||:||||
Db  228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYLTFGGGTKLEIK 273
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;
;
;     LENGTH: 241 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-235-838-11

Qy    Query Match
      Best Local Similarity  81.0%;           Score 455;   DB 1;   Length 241;
      Matches  84;  Conservative  10;  Pred. No. 2.3e-35;  Mismatches  11;  Indels  0;  Gaps  0;

Qy   1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
        |||:||||||||||:|:||||||||:||||:|  |||||||| ||:|||:|||||||||||||
Db 137  DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS  196

Qy  61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI  105
        ||||||||||:|:|:|||||||||||||:||| |||:|||||||:||
Db 197  RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYTFGGGTKLEI  241

RESULT 14
US-08-465-473B-11
Sequence 11, Application US/0846573B
Patent No. 5939531
; GENERAL INFORMATION:
;   APPLICANT: Wels, Winfried S.
;   APPLICANT: Hynes, Nancy E.
;   APPLICANT: Harwerth, Ina-Maria
;   APPLICANT: Groner, Bernd
;   APPLICANT: Hardman, No. 5939531man
;   APPLICANT: Zwickl, Markus
;   TITLE OF INVENTION: Recombinant Antibodies Specific for a
;   TITLE OF INVENTION: Growth Factor Receptor
;   NUMBER OF SEQUENCES: 34
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: NOVARTIS Corporation
;     STREET: 564 Morris Avenue
;     CITY: Summit
;     STATE: New Jersey
;     COUNTRY: USA
;     ZIP: 07901-6940
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/465,473B
;     FILING DATE: 5 June 1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/828,832
;     FILING DATE: 31-JAN-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 91-810079.3
;     FILING DATE: 05-FEB-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pfeifer, Hesna J.
;     REGISTRATION NUMBER: 22,640
;     REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (908)522 6940
;     TELEFAX: (908)522 6955
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 241 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-465-473B-11

Query Match
81.0%;           Score 455;   DB 2;   Length 241;
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      Best Local Similarity  80.0%;           Pred. No. 2.3e-35;  Mismatches  11;  Indels  0;  Gaps  0;
      Matches  84;  Conservative  10;

Qy   1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
        |||:||||||||||:|:||||||||:||||:|  |||||||| ||:|||:|||||||||||||
Db 137  DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS  196

Qy  61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI  105
        ||||||||||:|:|:|||||||||||||:||| |||:|||||||:||
Db 197  RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDLYTFGGGTKLEI  241

RESULT 15
US-08-602-725-29
Sequence 29, Application US/0860272725
Patent No. 5965710
; GENERAL INFORMATION:
;   APPLICANT: BODMER, WALTER F
;   APPLICANT: DURBIN, HELGA
;   APPLICANT: SNARY, DAVID
;   APPLICANT: STEWART, LORNA MD
;   APPLICANT: YOUNG, SUSAN
;   APPLICANT: BATES, PAUL A
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
;   TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: NIXON & VANDERHYE P.C.
;     STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
;     CITY: ARLINGTON
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22201
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/602,725
;     FILING DATE: 02-FEB-1996
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/GB94/01816
;     FILING DATE: 19-AUG-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9317423
;     FILING DATE: 21-AUG-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: SADOFF, B.J.
;     REGISTRATION NUMBER: 36663
;     REFERENCE/DOCKET NUMBER: 1090-8
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-816-4091
;     TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 29:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 108 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;     ORGANISM: Hukan REI light chain
US-08-602-725-29

Query Match
Best Local Similarity  80.9%;    83.0%;   Score 454.5;   DB 2;   Length 108;
Matches  88;  Conservative  8;  Pred. No. 1.1e-35;  Mismatches  9;  Indels  1;  Gaps  1;
```

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Qy     1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
          |||||||||||||||||||||||:  ||| |:|||||||||||:||: |  ||||| |:||
Db     1  DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLAWYQQTPGKAPKLLIYEASNLQAGVPS  60

Qy    61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI  105
          ||||||| ||| :|||||||||||||||| :|| :|||||||:||
Db    61  RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKIEI  106
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Search completed: May 7, 2002, 12:23:04
Job time: 175 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:31:42 ; Search time 67.26 Seconds
(without alignments)
304.462 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVFFLMAVVTGVNSE.........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627229 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length %	DB	ID	Description
1	589	79.0	468	11	Q99L31 mus musculu
2	494.5	66.3	473	11	Q99L25 mus musculu
3	480	64.3	109	11	Q92IC6 mus musculu
4	478	64.1	473	11	Q9JL85 mus musculu
5	425.5	57.0	463	11	Q99LC4 mus musculu
6	412	55.2	117	11	Q9qxe9 mus musculu
7	388.5	52.1	118	11	Q9ZIC4 mus musculu
8	387	51.9	117	11	Q9qxf0 mus musculu
9	383.5	51.4	110	11	Q9JL77 mus musculu
10	380	50.9	111	11	Q9d9b8 mus musculu
11	376.5	50.5	109	11	Q9JL75 mus musculu
12	375.5	50.3	114	11	Q9JL81 mus musculu
13	371.5	49.8	124	11	Q9u192 homo sapien
14	369	49.5	484	11	Q99La6 mus musculu
15	367	49.2	150	4	Q9Y298 homo sapien
16	366.5	49.1	500	4	Q9BRV0 homo sapien
17	361	48.4	157	4	Q95978 homo sapien
18	353	47.3	119	5	Q9GYZ2 schistosoma
19	350	46.9	119	4	Q9u194 homo sapien
20	348.5	46.7	110	11	Q9JL83 mus musculu
21	343	46.0	125	4	Q9UL95 homo sapien
22	340.5	45.6	487	11	Q99KA4 mus musculu
23	338	45.3		11	Q92IC6 mus musculu
24	324.5	43.5	116	4	Q9UL89 homo sapien
25	322.5	43.2	298	11	Q9QYF0 mus musculu
26	302.5	40.5	150	4	Q95973 homo sapien
27	301	40.3	120	4	Q9BUA1 homo sapien
28	295	39.5	597	11	Q9B0B8 homo sapien
29	294.5	39.5	118	4	Q9UL72 homo sapien
30	294	39.4	119	4	Q9UL73 homo sapien
31	294	39.4	597	11	Q9BU10 homo sapien
32	291.5	39.1	112	4	Q9HCC1 homo sapien
33	290	38.9	113	4	Q9UL90 homo sapien
34	285	38.2	131	4	Q9UL88 homo sapien
35	284.5	38.1	121	11	Q99NG4 homo sapien
36	281.5	37.7	147	4	Q9Y509 homo sapien
37	279	37.4	116	4	Q9UL93 homo sapien
38	279	37.4	479	11	Q99M22 homo sapien
39	275	36.9	121	4	Q9UL71 homo sapien
40	271.5	36.4	124	6	Q99ng4 homo sapien
41	269.5	36.1	124	6	Q9N0W6 oryctolagus
42	267.5	35.9	118	4	Q9N0W4 oryctolagus
43	265.5	35.6	122	4	Q9UL84 homo sapien
44	263.5	35.3	437	11	Q9R1A4 mus musculu
45	258.5	34.7	426	11	Q9DCD9 mus musculu

ALIGNMENTS

RESULT 1
Q99L31
ID   Q99L31   PRELIMINARY;   PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
SQ   SEQUENCE   468 AA;   51661 MW; 96352228B3332ADB CRC64;

Query Match 79.0%; Score 589; DB 11; Length 468;
Best Local Similarity 81.4%; Pred. No. 2.2e-51;
Matches 114; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |||||:||||||| ||||||||||||||||||:||||||||||||||||: :| ||||
Db   1 MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          |||||||:||| :|||:||||| |||||||||||||||||||||||||||:::||| :
Db   61 EQGLEWIGWIDPEDGETKYAPKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLL 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
          || |||:|:||:::||
Db 121 YGGY---YDYWGQGTTITV 136

RESULT 2
Q99L25
ID   Q99L25   PRELIMINARY;   PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)

DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
SQ   SEQUENCE   473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match   Best Local Similarity   66.3%;
Matches 96; Conservative 19; Pred. No. 8e-42;   Score 494.5; DB 11; Length 473;
Mismatches 24; Indels 3; Gaps 2;

Qy   1 MKCSWVWFFLMAVVGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP   60
         |: ||| | ||:|||||||||||||||||||||||||||||||||||| : | |||||||
Db   1 MEWSWVFLFLLSVTGVHSQVQLQQSDAELVKPGASVKLSCKVSGYTFTDHTIIHWVKQRP   60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATIIADTSSNTAYLQLSSLTSEDTAVYFCAREG- 119
         |||||||||:|:| |||||||||||||||||||||||||||||||||||||| :| ||
Db   61 EQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVFCSRGGS 120

Qy 120 -YYGNGVYAMDYWGQGTSVTV 140
          ||| ||| ||||||||||:||
Db 121 IYYG-YGLYFDYWGQGTTITV 141

RESULT   3
ID   Q9JL85   PRELIMINARY;   PRT;   109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF206021; AAF69319.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
SQ   SEQUENCE   109 AA; 11944 MW; DFE615F86CED4EDE CRC64;

Query Match   Best Local Similarity   64.3%;   Score 480; DB 11; Length 109;
Matches 91; Conservative 8; Mismatches 8; Indels 6; Gaps 1; Pred. No. 3.8e-41;

Qy   28 AELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKA   87
         |||||||||||||||||||||| :||||||||||||||||||| |||||||||||||
Db   1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKVDPKFQGKA   60

Qy   88 TIPADTSSNTAYLQLSSLTSEDTAVYFCAREGYGYGNYGVYAMDYWGQGTSVTV 140
         ||:|||||||||||||||||||||||:|:| |||||||||||||::|
Db   61 TITSDTSSNTAYLQLSSLTSEDTAVYCVRR------GAVVFDYWGQGTALTV 107

RESULT   4
ID   Q9D8L4   PRELIMINARY;   PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1810060009RIK PROTEIN.
GN   1810060009RIK
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AK007918; BAB25349.1; -.
DR   MGD; MGI:1924014; 1810060009Rik.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IgC1; 2.
DR   SMART; SM00407; IgC1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match   Best Local Similarity   64.1%;   Score 478; DB 11; Length 473;
Matches 94; Conservative 19; Mismatches 23; Indels 4; Gaps 2; Pred. No. 3.7e-40;

Qy   1 MKCSWVWFFLMAVVGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP   60
         |: ||| | | | ||||||||||||||||||||||||||:||||:|||: | |||||||
Db   1 MEWSWVFLFLLSVTAGVHCQVQLQQSGAELVKPGASVKISCKASGYTFTDYINWVKQRP   60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATIIADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
         ||||||| :|:| ||||:|:||||||||:|||:||||||:||||||||:||||||:||
Db   61 GQGLEWIGKLGPGSSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVFCARSGY 120

Qy 121 YGNGVYAMDYWGQGTSVTV 140
           |||:|||||||||||:||
Db 121 --DYDWFA---YWGQGTLVTV 136

RESULT 5

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ID   Q99LC4
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;
```

PRELIMINARY;   PRT;   463 AA.

Query Match   57.0%; Score 425.5; DB 11; Length 463;
Best Local Similarity   59.3%; Pred. No. 7.3e-35;
  Matches   83; Conservative   21; Mismatches 33; Indels   3; Gaps   2;

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Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
Db    1 MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVKLSCKASGYTFTGYGVSWVKQRT 60

Qy   61 EQGLEWIGRIDPANGYTRKYDPKFQGKARITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
Db   61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
Db  121 Y-SYDLFA--YWGQGTLVTV 137
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RESULT 6

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ID   Q9QXE9
AC   Q9QXE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ225174; CAB65237.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1
FT   NON_TER     117
SQ   SEQUENCE   117 AA;  13000 MW;  CDDE2AF84D499734 CRC64;
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PRELIMINARY;   PRT;   117 AA.

Query Match   55.2%; Score 412; DB 11; Length 117;
Best Local Similarity   66.9%; Pred. No. 3.1e-34;
  Matches   81; Conservative   14; Mismatches 20; Indels   6; Gaps   1;

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Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
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Db    1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   80 DPKFQGKARITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY------YAMDYWGQGTSVT 114

Qy  140 V 140
Db  115 V 115
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RESULT 7

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ID   Q9Z1C4
AC   Q9Z1C4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA   Matis L.M., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; U78801; AAD00293.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1
FT   NON_TER     118
SQ   SEQUENCE   118 AA;  13036 MW;  90EEC559D31EC4FC CRC64;
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PRELIMINARY;   PRT;   118 AA.

Query Match   52.1%; Score 388.5; DB 11; Length 118;
Best Local Similarity   62.1%; Pred. No. 7.5e-32;
  Matches   77; Conservative   16; Mismatches 20; Indels   11; Gaps   2;

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Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
Db    1 QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60

Qy   80 DPKFQGKARITADTSSNTAYLQLSSLTSEDTAVYFCARE---GYYGNYGVYAMDYWGQGT 136
Db   61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYF------DYWGQGT 112

Qy  137 SVTV 140
Db  113 TLTV 116
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RESULT 8

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ID   Q9QXF0
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```

PRELIMINARY;   PRT;   117 AA.

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   117 AA;  13060 MW;  D816AD085A47E4C CRC64;

Query Match             Best Local Similarity   51.9%;
                        Score 387; DB 11; Length 117;
Matches   77;  Conservative  16;  Mismatches  21;  Indels  8;  Gaps  2;   Pred. No. 1e-31;

Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
         | | ||::||||||||||::||:|||  |:| |:|  |:|  | || ||| | |  ::|
Db    1 EVQLQQSGPELVKPGASVKMSCKASGYTFDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCARE-GYYGNYGVYAMDYWCQGTSV 138
         :||:|||:| ||:||||||||||||||||:||:||||::||  |::          :::
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDY------FDYWGQGTTL 113

Qy  139 TV 140
         ||
Db  114 TV 115


RESULT 9
ID   Q9JL77      PRELIMINARY;      PRT;   110 AA.
AC   Q9JL77;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206029; AAF69327.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
SQ   SEQUENCE   110 AA;  12138 MW;  2EDE81FB58G2C9AF CRC64;

Query Match             Best Local Similarity   65.8%;
                        Score 383.5; DB 11; Length 110;
Matches   73;  Conservative  15;  Mismatches  18;  Indels  5;  Gaps  1;   Pred. No. 2.2e-31;

Qy   30 LVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDRFQGKAII 89
         :|||||||||||:|||:| ::::   ::|||| ||||||| ||| ||| ||: ||||:|
Db    3 VRPGASVKLSCKASGYTFTSSWMHWAKQRPGQGLEWIGEIHPNSGHTNYNEKFKGKATL 62

Qy   90 TADTSSNTAYLQLSSLTSEDTAVFCAREGYCNYGVYAMDYWCQGTSVTV 140
```

```
Db   63 TVDISSSTAYVDLSSLTSEDSAVYYCARQRRN-----YAMDYWGGTSVTV 108


RESULT 10
ID   Q9D9B8      PRELIMINARY;      PRT;   111 AA.
AC   Q9D9B8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:1700110I11, FULL INSERT SEQUENCE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TESTIS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AK007163; BAB24877.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   111 AA;  11976 MW;  874DDF7BD9BD7B2 CRC64;

Query Match             Best Local Similarity   50.9%;
                        Score 380; DB 11; Length 111;
Matches   73;  Conservative  17;  Mismatches  14;  Indels  0;  Gaps  0;   Pred. No. 5e-31;

Qy   14 VTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPA 73
         :|||:|:||||||||.||||||||||||:|||:|  :::  ::||||| ::||||||  |
Db    1 MTGVHSQVQLQQSGPELVKPGASVKLSCKASGYAFSSSWMNWVKQRPGKGLEWIGRIYPG 60

Qy   74 NGYTKYDPKFQGKAIITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
         :| | ||:|:|||| |||:||:|||||||||||||||:|||||| 
Db   61 DGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR 104


RESULT 11
ID   Q9JL75      PRELIMINARY;      PRT;   109 AA.
AC   Q9JL75;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
```

RESULT 12
Q9JL81

```
ID   Q9JL81       PRELIMINARY;      PRT;   114 AA.
AC   Q9JL81;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206025; AAF69323.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12829 MW;  404885FDE6BA56F8 CRC64;
```

Query Match   50.3%; Score 375.5; DB 11; Length 114;
Best Local Similarity   61.6%; Pred. No. 1.5e-30;
Matches 69; Conservative 21; Mismatches 21; Indels   1; Gaps   1;

```
Qy   29 ELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKAT 88
        ||||||||||:|:||||:||::||||||| ||||||||:|||:|:||:::|:::||:|||
Db    2 QLVRPGASVKISCKASGYSFTSYWMHWVQKQRPGQGLEWIGMIDPSDSETRLNQKFKDKAT 61
Qy   89 ITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
        :||| :||||:|||:||||||:||||||| :|| :|||||||||||||
Db   62 LTVDKSSSTAYMQLSSPTSEDSAVYYCARSNYYGS-SLYYFDYWGQGTTLTV 112
```

Q9JL81

```
ID   Q9JL81       PRELIMINARY;      PRT;   114 AA.
AC   Q9JL81;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206031; AAF69929.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  12118 MW;  FF65E441BBF936A6 CRC64;
```

Query Match   50.5%; Score 376.5; DB 11; Length 109;
Best Local Similarity   63.4%; Pred. No. 1.e-30;
Matches 71; Conservative 18; Mismatches 18; Indels   5; Gaps   1;

```
Qy   29 ELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKAT 88
        |||||||||:|:||:||::|||||||||| ||||||||:||:|:|||::|:::||:|||
Db    1 ELVKPGASVKMSCKASGYTFTSYMHWVKQRPGQGLEWIGYINPYNDGTKYNEKFKGKAT 60
Qy   89 ITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
        :|||: |||||::||:||||||:|||||||| |||||::|||||||||||
Db   61 LTSDKSSSTAYMELSSLTSEDSAVYYCARDGNYRGF-------DYWGQGTTLTV 107
```

RESULT 13
Q9UL92

```
ID   Q9UL92       PRELIMINARY;      PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035022; AAD56258.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;
```

Query Match   49.8%; Score 371.5; DB 4; Length 124;
Best Local Similarity   56.6%; Pred. No. 4.1e-30;
Matches 73; Conservative 18; Mismatches 23; Indels 15; Gaps   2;

```
Qy   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
        ||||:.|||:||||||||:|:||||:|:|||:||:.|::|.:||||||.||:.|.:...|
Db    1 EVQLVESGAEVKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60
Qy   80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAM------DY 131
        ..|||..|.:|.||:.:|.|::|||:||||.|||:|||.-------.|.::.|||.|:|
Db   61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR-------GLYVVVPAAFSRFDY 113
Qy  132 WGQGTSVTV 140
        ||||| |||
Db  114 WGQGTLVTV 122
```

RESULT 14
Q99LA6

```
ID   Q99LA6       PRELIMINARY;      PRT;   484 AA.
AC   Q99LA6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:6319).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC    TISSUE=MAMMARY TUMOR;
RA    Strausberg R.;
RL    Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; BC003495; AAH03495.1; -.
SQ    SEQUENCE  484 AA;  52567 MW;  8EAEA4F9BCF582FA CRC64;

Query Match
Best Local Similarity    49.5%;   Score 369;  DB 11;  Length 484;
Matches  67;  Conservative 28;  Mismatches 39;  Indels  2;  Gaps  1;

Qy    5  WVMFFLMAAVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL  64
            | : |||||   :  ::::|| ||| ||| ||  | ::|:||| ||  : ||| | : ||
Db    5  WTLLFLMAAAQSIQAQIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKGL  64

Qy   65  EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNY  124
            :|:| :|: | | |||||||:|  :|:|:||::||| | ||||||||||| |  : |
Db   65  KWMGWVNIETGESVYADDFKGRFAFSLETSASTIHLQINNLKNEDTATYFCARSDY--DY  122

Qy  125  GVYAMDYWGQGTSVTV 140
            :||||||||||||||||
Db  123  DIYAMDYWGQGTSVTV 138

RESULT 15
ID    Q9Y298
AC    Q9Y298;
DT    01-NOV-1999 (TrEMBLrel. 12, Created)
DT    01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT    01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE    IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN    IGG VH.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=98322115; PubMed=9657749;
RA    Jacquemin M.G., Vander Elst L.P.L.;
RT    "Mechanism and kinetics of factor VIII inactivation: study with an
RT    IgG4 monoclonal antibody derived from a hemophilia A patient with
RT    inhibitor.";
RL    Blood 92:496-506(1998).
CC    -!-  SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC         DOMAIN.
DR    EMBL; AJ224083; CAA11829.1; -.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_V.
DR    Pfam; PF00047; ig; 1.
DR    SMART; SM00406; IGv; 1.
KW    Signal.
FT    SIGNAL       1     19
FT    NON_TER      1
SQ    SEQUENCE  150 AA;  16031 MW;  563D164AB22802D5 CRC64;

Query Match
Best Local Similarity    51.4%;   Score 367;  DB 4;  Length 150;
Matches  72;  Conservative 24;  Mismatches 38;  Indels  6;  Gaps  1;

Qy    1  MKCSWVMFFLMAAVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP  60
            : | |||||||||   ::|| || ||||:||| ||| |||| :| ::|:||  : |||
Db    1  MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHHWVGQAP  60

Qy   61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            : |||:|| |:| ||| |  :|||  |||| ::|:|:|:| |||||||||||| |||||:|
Db   61  GKGLEWVGSFPDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-- 118

Qy  121  YGNYGVYAMDYWGQGTSVTV 140
            | | ||||||||||||||||
Db  119  ----?PDAFDIWGQGTMVTV 134
```

GenCore version 4.5
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OM protein - protein search using sw model

Run on: May 7, 2002, 12:23:47 ; Search time 37.68 Seconds
                                          (without alignments)
                                          214.291 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT...........YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_68:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	488	86.8	104	2	S26330	Ig kappa chain V r
2	479	85.2	104	2	S26329	Ig kappa chain V r
3	478	85.1	106	2	S31981	Ig kappa chain V r
4	463.5	82.5	125	2	C33936	Ig kappa chain V r
5	452	80.4	97	2	S09365	Ig kappa chain - m
6	446.5	79.4	107	2	PH1064	Ig kappa chain V r
7	443.5	78.9	108	1	PL0270	Ig kappa chain V r
8	443.5	78.9	129	2	K1HURE	Ig kappa chain V r
9	443	78.8	103	2	S52789	Ig kappa chain V r
10	440.5	78.4	107	2	S26332	Ig light chain V r
11	440	78.3	94	2	PL0272	Ig light chain V r
12	439.5	78.2	107	2	E33730	Ig kappa chain V r
13	439.5	78.2	107	2	PL0271	Ig kappa chain V r
14	439.5	78.2	108	1	K1HUAU	Ig kappa chain V r
15	435.5	77.5	108	2	I39154	Ig kappa chain (BR
16	429.5	76.4	110	2	S44118	Ig kappa chain V-J
17	429.5	76.4	127	2	S40367	Ig kappa chain V-J
18	426	75.8	107	2	S36275	Ig lambda chain V
19	424.5	75.5	125	2	S40333	Ig kappa chain V-J
20	421.5	75.0	108	1	K1HULY	Ig kappa chain V-I
21	421.5	74.9	108	1	K1HUAG	Ig kappa chain V-I
22	419.5	74.6	108	1	K1HURY	Ig kappa chain V-I
23	419.5	74.5	123	2	S40331	Ig kappa chain - h
24	418.5	74.4	109	2	S31998	Ig kappa chain - h
25	415.5	73.9	131	2	S40352	Ig kappa chain V-J
26	414.5	73.8	131	2	S40336	Ig kappa chain V-J
27	414	73.7	124	2	S40336	Ig kappa chain V-I
28	413.5	73.6	108	1	K1HUSW	Ig kappa chain V r
29	412.5	73.4	108	2	B49047	Ig kappa chain V r
	412	73.3	106	2	PC2397	anti-tetanus toxin

30	410.5	73.0	108	2	S44122	Ig kappa chain V r
31	410.5	73.0	109	2	S31981	Ig kappa chain - h
32	409.5	72.9	129	1	K1HUWK	Ig kappa chain V r
33	409	72.8	107	1	K1HUAR	Ig kappa chain pre
34	408.5	72.8	108	1	K1HUWE	Ig kappa chain V-I
35	408.5	72.7	139	2	S40365	Ig kappa chain - h
36	407.5	72.5	141	2	A49134	Ig kappa chain V-I
37	405.5	72.2	117	2	S46371	Ig kappa chain V-J
38	405	72.1	108	2	S30521	Ig kappa chain - h
39	404.5	72.0	132	2	S40334	Ig kappa chain V-J
40	404	71.8	94	2	S12240	Ig light chain V-I
41	403.5	71.8	107	2	S36264	Ig kappa chain V r
42	403.5	71.8	127	2	S43528	Ig kappa chain V r
43	403	71.7	108	2	S42263	Ig kappa chain V r
44	403	71.7	117	2	PH1063	Ig kappa chain V r
45	402.5	71.6	108	1	K1HUHU	Ig kappa chain V-I

ALIGNMENTS

RESULT   1
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26330
A;Accession: S26330
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match   86.8%;   Score 488;   DB 2;   Length 104;
Best Local Similarity   85.6%;   Pred. No. 1.3e-35;
Matches   89;   Conservative   8;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTICCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||:| |||||||:| ||||||:|:|||| |||||||||||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
          |||||||||||||||||:|:|||||||||||||||||||||:||:|
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104

RESULT   2
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26329
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

RESULT 3
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
R;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
J. Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Reference number: A33936; MUID:89282831
A;Accession: C33936
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   85.2%;   Score 479; DB 2; Length 104;
Matches 88; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
        ||||||||||||:|:|:||||||||||||||||||||||||:|:|
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104

Query Match
Best Local Similarity   83.0%;   Score 478; DB 2; Length 106;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db   1 DIQMTQSPSSLSASLGGKVVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
Db   61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106

Query Match
Best Local Similarity   82.5%;   Score 463.5; DB 2; Length 125;
Matches 89; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

RESULT 4
S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Pedersen, R.; Van Ness, B.
R;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segm
Nucleic Acids Res. 17, 9797-9809, 1989
A;Reference number: S09365; MUID:90098044
A;Accession: S09365
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   83.2%;   DB 2; Length 125;
Matches 89; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db   18 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 77

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        ||||||||||||:|:|:|||||||||||||||||||:|||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLRTFGGGTKLEIK 124

RESULT 5
PHI064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PHI064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PHO971; MUID:92381444
A;Accession: PHI064
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   80.4%;   Score 452; DB 2; Length 97;
Matches 83; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKACKGPRLLIWYTSTLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTE 97

RESULT 6
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match
Best Local Similarity   79.4%;   Score 446.5; DB 2; Length 107;
Matches 85; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db   1 DIQMTQSPSSLSASLGDKVTITCRTSQDISKNMAWYQHKACKGPRLLIWYTSTLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTE 97

```
              |||||||||||||  ||||||||||||||||||||||||||||  ||| :|||
Db    61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQDKVPYTFGSGTKLEIK 107
```

RESULT 7
KIHURE
Ig kappa chain V-I region (Rel) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A91663; A01873
R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunoglobulin-L-Kette vom k
vollstaendige Aminosaeuresequenz des Proteins.
A;Reference number: A91663; MUID:7602758
A;Accession: A91663
A;Molecule type: protein
A;Residues: 1-108 <PAL>
A;Note: the C region of this chain has the Inv (1,2) marker
R;Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the variable portions of the Ben
A;Reference number: A90392; MUID:76039968
C;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
A;Comment: This is a Bence Jones protein.
C;Genetics:
C;Gene: GDB:IGKV1
A;Cross-references: GDB:135264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental

```
Query Match       78.9%;
Best Local Similarity   81.1%;  Score 443.5;  DB 1;  Length 108;
Matches   86;  Conservative   9;  Pred. No. 9.4e-32;
  Mismatches  10;  Indels  1;  Gaps  1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||:||||||||||||  |||  |||| |||||||||||||||:||||||||||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQDYNL-WTFGQGTRVEI 105
         ||||||||| |||||||||||||||||||||||| :|||||||::|
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
```

RESULT 8
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

```
Query Match       78.9%;
Best Local Similarity   79.4%;  Score 443.5;  DB 2;  Length 129;
Matches   85;  Conservative  10;  Pred. No. 1.1e-31;
  Mismatches  11;  Indels  1;  Gaps  1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||:||||||||||||  |||  |||| |||||||||||||||:||||||||||
Db   23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNNYQQKPGKAPKLLIHAASSLETGVPS 82

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQDYNL-WTFGQGTRVEIK 106
         ||||||||| |:||||||||||| |||  |||| ||| ||||||||:|
Db   83 RFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGGGTKVEIK 129
```

RESULT 9
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59187; NID:g53318; PIDN:CAA41897.1; PID:g134064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g53221; PIDN:CAA41901.1; PID:g134066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```
Query Match       78.8%;
Best Local Similarity   77.7%;  Score 443;  DB 2;  Length 103;
Matches   80;  Conservative  13;  Pred. No. 9.9e-32;
  Mismatches  10;  Indels  0;  Gaps  0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||:|||||  |  ||| ||| ||| |||||| ||||| ||:||:||||||||
Db    1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQDYNLWTFGQGTKV 103
         ||||||||| |||||||||||||||||| :||||| |||||||
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYYCLQYDNLWTFGGGTKL 103
```

RESULT 10
PL0272
Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

RESULT 11

```
Query Match   78.4%;  Score 440.5;  DB 2;  Length 107;
Best Local Similarity 78.5%;
Matches   84;  Conservative  11;  Mismatches  11;  Indels   1;  Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMANYQQTPGKAPRLLIHYTSALQPGIPS  60
        |||||||| :|||||::|| :||| |||||::|:||||| ||:| |||||| |||: |||||
Db   1 DIQMTQSPCSLSASLGDKVIITCRTSQDISKNMANYQHKAGKGPRLLIWYTSTLQPGIPS  60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||||||| | :|| | :||||||||||||:  | ||| ||:|||
Db  61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
```

E3730

Ig kappa chain V region (9.42) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990
C;Accession: E3730
R;Lawler, A.M.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli...
A;Reference number: A33730; MUID:89367325
A;Accession: E3730
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: GB:M26000; NID:g197119; PIDN:AAA38916.1; PID:g197120
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

RESULT 12

```
Query Match   78.3%;  Score 440.;  DB 2;  Length 94;
Best Local Similarity 86.2%;  Pred. No. 1.6e-31;
Matches   81;  Conservative   7;  Mismatches   6;  Indels   0;  Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMANYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||:|| || ||||:|||||| |:|||:| |||||||||||: |||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSILQPGIPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL 94
        ||||||||||||||||||||||||||||||||||
Db  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL 94
```

PL0269

Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic...
A;Reference number: PL0231; MUID:9011618
A;Accession: PL0269
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

RESULT 13

```
Query Match   78.2%;  Score 439.5;  DB 2;  Length 107;
Best Local Similarity 84;  Conservative  10;  Pred. No. 2.1e-31;
Matches   84;  Conservative  10;  Mismatches  12;  Indels   1;  Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMANYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||| :|||||::|| : |||||||:|:||||| ||:| |||||| |||: |||||||
Db   1 DIQMTQSPCSLSASLGDKVIIACRTSQDIRKNMANYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||||||| | :|| | :||||||||||||:  | ||| ||:|||
Db  61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
```

PL0271

Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic...
A;Reference number: PL0231; MUID:9011618
A;Accession: PL0271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

RESULT 14

```
Query Match   78.2%;  Score 439.5;  DB 2;  Length 107;
Best Local Similarity 84;  Conservative  10;  Pred. No. 2.1e-31;
Matches   84;  Conservative  10;  Mismatches  12;  Indels   1;  Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMANYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||| :|||||::|| :||| ||||:|:||||| ||:| |||||| |||: |||||||
Db   1 DIQMTQSPCSLSASLGDKVIITCRTSQDIRKNMANYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||||||| | :|| | :||||||||||||:  | ||| ||:|||
Db  61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
```

K1HUAU

Ig kappa chain V-I region (Au) - human

C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, ...
A;Reference number: A91653; MUID:72189444
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; S...
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones prote...
A;Reference number: A90729; MUID:77022433
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances ...

A;Reference number: S02572; MUID:88005152
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

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Query Match          78.2%;   Score 439.5; DB 1;   Length 108;
Best Local Similarity  79.4%;  Pred. No. 2.1e-31;
Matches    85;  Conservative   8; Mismatches  13; Indels   1; Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||||||| ||||| |: ||||| | ||||||:|||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          |||| ||| :||||||||||||||||||| | |||||||||||
Db   61 RFSGSGSGAHFTFTISSLQPEDIATYYCQQYDVLPWTFGQGTKVEIK 107
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RESULT 15
I39154

Ig kappa chain (BRE) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: I39154
R;Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A;Reference number: I39154; MUID:96003804
A;Accession: I39154
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-108 <RES>
A;Cross-references: EMBL:U31344; NID:g944925; PIDN:AAA79238.1; PID:g944926
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

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Query Match          77.5%;   Score 435.5; DB 2;   Length 108;
Best Local Similarity  79.4%;  Pred. No. 4.6e-31;
Matches    85;  Conservative   9; Mismatches  12; Indels   1; Gaps   1;

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          ||||||||||||||||||||||||||| ||||| |:||||| | ||||||:|||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          |||| ||| :|||||||||||||||||| | |||||||||||
Db   61 RFSGSGSGTEYTFTISSLQPEDIATYYCQQYDDLPYTFGQGTKVEIK 107
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Search completed: May 7, 2002, 12:23:47
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:34 ; Search time 21.92 Seconds
                                          (without alignments)
                                          177.303 Million cell updates/sec

Title: us-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.............YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	443.5	78.9	108	1	KV1O_HUMAN	P01607 homo sapien
2	439.5	78.2	108	1	KV1B_HUMAN	P01594 homo sapien
3	421.5	75.0	108	1	KV1M_HUMAN	P01601 homo sapien
4	419.5	74.6	108	1	KV1A_HUMAN	P01593 homo sapien
5	419.5	74.6	108	1	KV1P_HUMAN	P01608 homo sapien
6	419.5	74.5	108	1	KV1Y_HUMAN	P01609 homo sapien
7	413.5	74.6	108	1	KV1Y_HUMAN	P80362 homo sapien
8	413.5	73.6	108	1	KV1D_HUMAN	P01596 homo sapien
9	409.5	72.9	129	1	KV1W_HUMAN	P04431 homo sapien
10	409	72.8	107	1	KV1N_HUMAN	P01605 homo sapien
11	408	72.7	108	1	KV1R_HUMAN	P04430 homo sapien
12	402.5	71.6	108	1	KV1F_HUMAN	P01597 homo sapien
13	397.5	70.7	108	1	KV1H_HUMAN	P01603 homo sapien
14	396.5	70.6	108	1	KV1V_HUMAN	P01611 homo sapien
15	390.5	69.5	108	1	KV1K_HUMAN	P06314 homo sapien
16	388.5	69.1	108	1	KV1E_HUMAN	P04432 homo sapien
17	388.5	68.8	108	1	KV1L_HUMAN	P01599 homo sapien
18	386.5	68.6	108	1	KV1C_HUMAN	P01600 homo sapien
19	385.5	68.4	108	1	KV1G_HUMAN	P01598 homo sapien
20	384.5	68.2	108	1	KV1X_HUMAN	P01600 homo sapien
21	384.5	68.2	108	1	KV1S_HUMAN	P01610 homo sapien
22	383.5	68.2	108	1	KV4C_HUMAN	P01595 homo sapien
23	383.5	67.9	129	1	KV5J_MOUSE	P01596 homo sapien
24	381.5	67.0	134	1	KV1J_HUMAN	P01604 homo sapien
25	376.5	66.1	117	1	KV5E_MOUSE	P01606 mus musculu
26	371.5	65.5	128	1	KV4B_HUMAN	P01602 homo sapien
27	368	65.2	117	1	KV5O_MOUSE	P01602 mus musculu
28	366.5	64.9	133	1	KV5N_MOUSE	P01643 mus musculu
29	365	64.9	117	1	KV4B_HUMAN	P01637 homo sapien
30	364.5	64.9	128	1	KV5E_MOUSE	P06313 mus musculu
31	363.5	64.7	108	1	KV5O_MOUSE	P01648 mus musculu
32	362	64.7	108	1	KV5N_MOUSE	P01647 mus musculu
33	362	64.4	108	1	KV1T_HUMAN	P01612 homo sapien
34	361.5	64.4	109	1	KV1I_HUMAN	P01601 homo sapien
35	361.5	64.3	117	1	KV5M_MOUSE	P01644 mus musculu
36	359.5	64.0	108	1	KV5K_MOUSE	P01646 mus musculu
37	358.5	63.8	108	1	KV5L_MOUSE	P01645 mus musculu
38	356.5	63.4	112	1	KV1U_HUMAN	P01613 homo sapien
39	348.5	62.0	114	1	KV4A_HUMAN	P01625 homo sapien
40	348	61.9	129	1	KV3H_HUMAN	P04207 homo sapien
41	346	61.6	129	1	KV3M_HUMAN	P18136 homo sapien
42	345.5	61.5	108	1	KV5T_MOUSE	P01653 mus musculu
43	345	61.5	108	1	KV5F_MOUSE	P01638 mus musculu
44	341.5	61.4	115	1	KV3E_HUMAN	P01623 homo sapien
45	341	60.8	109	1	KV5Q_MOUSE	P01650 mus musculu

(additional listed entries)

	340.5	60.7	108	1	KV5S_MOUSE	P01652 mus musculu
	340.5	60.6	108	1	KV5U_MOUSE	P04946 mus musculu
	339.5	60.4	108	1	KV3D_HUMAN	P01622 homo sapien
	339	60.3	108	1	KV3F_HUMAN	P01624 homo sapien

ALIGNMENTS

RESULT 1
KV1O_HUMAN
ID   KV1O_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION REI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup V-I (Bence-Jones protein Rei.) isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC   MARKER.
DR   PIR; A01873; KIHURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88
FT   STRAND   4   7
FT   STRAND   10   13
FT   TURN   15   16
FT   STRAND   19   25
FT   TURN   30   31
FT   STRAND   33   38
FT   STRAND   40   41
FT   TURN   45   49

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FT   TURN           50     52
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FT   TURN           56     57
FT   TURN           56     57
FT   STRAND         60     61
FT   TURN           62     67
FT   STRAND         68     69
FT   TURN           70     75
FT   HELIX          80     82
FT   STRAND         85     90
FT   STRAND         98     98
FT   STRAND        102    106
FT   NON_TER       108    108
SQ   SEQUENCE      108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

Query Match
Best Local Similarity   78.9%;   Score 443.5; DB 1;  Length 108;
Matches  86;  Conservative   9;  Mismatches  10;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDIINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||: |:||||:|| ||||||||||:|||:|  :: |:|:||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
          ||||||| |||||||||||||||||| || |:| |:||||||||:|
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
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RESULT 2
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ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "the structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; KIHUAU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN          1     23    FRAMEWORK 1.
FT   DOMAIN         24     34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN         35     49    FRAMEWORK 2.
FT   DOMAIN         50     56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN         57     88    FRAMEWORK 3.
FT   DOMAIN         89     97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN         98    107    FRAMEWORK 4.
FT   DISULFID       23     88    BY SIMILARITY.
FT   NON_TER       108    108
SQ   SEQUENCE      108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

Query Match
Best Local Similarity   78.2%;   Score 439.5; DB 1;  Length 108;
Matches  85;  Conservative   8;  Mismatches  13;  Indels   1;  Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDIINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||: :||||  ||||||:|||||:|||:|  :: |:||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDIDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          ||||||| |:||||||||||||||||| ||| |:| |||||||||||
Db   61 RFSGSGSGAHFTFTISSLQPEDIATYYCQQYDLPWTFGQGTKVEIK 107
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RESULT 3
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ID   KV1M_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION LAY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
RN   [2]
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; KIHULY.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN          1     23    FRAMEWORK 1.
FT   DOMAIN         24     34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN         35     49    FRAMEWORK 2.
FT   DOMAIN         50     56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN         57     88    FRAMEWORK 3.
FT   DOMAIN         89     97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN         98    107    FRAMEWORK 4.
FT   DISULFID       23     88    BY SIMILARITY.
FT   NON_TER       108    108
SQ   SEQUENCE      108 AA;  11834 MW;  739993A95431434A CRC64;

Query Match
Best Local Similarity   75.0%;   Score 421.5; DB 1;  Length 108;
Matches  81;  Conservative  11;  Mismatches  13;  Indels   3;  Gaps   2;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDIINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||:||||||||||: :||  :| |||||:||| |||:|||:| :: ||:||
Db    1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNVLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
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RESULT 4
KV1A_HUMAN
ID   KV1A_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=6924734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein, 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; KIHUAG.
HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match   74.6%; Score 419.5; DB 1; Length 108;
Best Local Similarity   76.6%; Pred. No. 1.9e-37;
Matches   82; Conservative   9; Mismatches 15; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         ||||||||||||||||||||||| |||||| | ||||: |:||| ||:| :|: || ||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQOGPKKAPKILIYDASNLETGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         |||||||| ||:||||| |||||||||| ||:: | :||||||| :|
Db   61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107

RESULT 5
KV1P_HUMAN
ID   KV1P_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION ROY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;

RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RT   "(In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC   MARKER.
DR   PIR; A01874; KIHURY.
HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match   74.6%; Score 419.5; DB 1; Length 108;
Best Local Similarity   75.7%; Pred. No. 1.9e-37;
Matches   81; Conservative   12; Mismatches 13; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||| :|||||| | |||| : |:|| | :| :|: || ||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKILIYDASKLEAGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         ||||||| :|:||||| |||||||||| ||: | :||||||| :|
Db   61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDNLPLTFGGGTKVDFK 107

RESULT 6
KV1Y_HUMAN
ID   KV1Y_HUMAN   STANDARD;   PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7793911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";

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RL       J. Mol. Biol. 147:185-193(1981).
CC       -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR       PDB; 1WTL; 01-NOV-94.
DR       InterPro; IPR003006; Ig_MHC.
DR       InterPro; IPR003596; Ig_v.
DR       Pfam; PF00047; ig; 1.
DR       SMART; SM00406; IGv; 1.
KW       Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT       DOMAIN         1     23       FRAMEWORK 1.
FT       DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT       DOMAIN        35     49       FRAMEWORK 2.
FT       DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT       DOMAIN        57     88       FRAMEWORK 3.
FT       DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT       DOMAIN        98    107       FRAMEWORK 4.
FT       DISULFID      23     88
FT       CONFLICT      30     31       TN -> SD (IN REF. 2).
FT       NON_TER      108    108
SQ       SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;

Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
Best Local Similarity   75.7%;  Pred. No.1.9e-37;
Matches    81;  Conservative   11;  Mismatches   14;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||||: :|| |:::|||||||||||||:||:|||:|||||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQDINKYMANYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         ||||||:||| ||||||||||||||||:||:|| ||:||||||:||
Db   61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNL-WTFGQGTKVDIK 107

RESULT 7
ID       KV1Q_HUMAN     STANDARD;      PRT;   108 AA.
AC       P01609;
DT       21-JUL-1986 (Rel. 01, Created)
DT       21-JUL-1986 (Rel. 01, Last sequence update)
DT       15-JUL-1999 (Rel. 38, Last annotation update)
DE       IG KAPPA CHAIN V-I REGION SCW.
OS       Homo sapiens (Human).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX       NCBI_TaxID=9606;
RN       [1]
RP       SEQUENCE.
RX       MEDLINE=75052271; PubMed=4435756;
RA       Eulitz M., Hilschmann N.;
RT       "The primary structure of a human immunoglobulin L-chain of
RT       kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides
RT       and the complete amino acid sequence.";
RL       Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC       -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC       -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC           MARKER.
DR       PIR; A01875; K1HUSW.
DR       HSSP; P01607; 1REI.
DR       InterPro; IPR003006; Ig_MHC.
DR       InterPro; IPR003596; Ig_v.
DR       Pfam; PF00047; ig; 1.
DR       SMART; SM00406; IGv; 1.
KW       Immunoglobulin V region; Bence-Jones protein.
FT       DOMAIN         1     23       FRAMEWORK 1.
FT       DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT       DOMAIN        35     49       FRAMEWORK 2.
FT       DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT       DOMAIN        57     88       FRAMEWORK 3.
FT       DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT       DOMAIN        98    107       FRAMEWORK 4.
FT       DISULFID      23     88       BY SIMILARITY.
FT       NON_TER      108    108
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SQ       SEQUENCE   108 AA;  11764 MW;  32CECDDF9644414 CRC64;

Query Match             73.6%;  Score 413.5;  DB 1;  Length 108;
Best Local Similarity   74.8%;  Pred. No.8.1e-37;
Matches    80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||||: :||  :::|||||||||||||:||:|||:|||||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDIRKIHLNWYDQKPGKAPKLLIYGASILETGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
         ||||||:|||:|| :||||||||||||:||:|| | |||||||:||
Db   61 RFSGSGSGTDFLTISSLQPEDIATYYCQQYDNVPITFGQGTRVENK 107

RESULT 8
ID       KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC       P04431;
DT       13-AUG-1987 (Rel. 05, Created)
DT       13-AUG-1987 (Rel. 05, Last sequence update)
DT       15-JUL-1999 (Rel. 38, Last annotation update)
DE       IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS       Homo sapiens (Human).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX       NCBI_TaxID=9606;
RN       [1]
RP       SEQUENCE FROM N.A.
RX       MEDLINE=85014148; PubMed=6091049;
RA       Klobeck H.G., Combriato G., Zachau H.G.;
RT       "Immunoglobulin genes of the kappa light chain type from two human
RT       lymphoid cell lines are closely related.";
RL       Nucleic Acids Res. 12:6995-7006(1984).
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DR       EMBL; X00965; CAA25477.1; ALT_TERM.
DR       PIR; A01883; K1HUWK.
DR       HSSP; P01607; 1REI.
DR       InterPro; IPR003006; Ig_MHC.
DR       InterPro; IPR003596; Ig_v.
DR       Pfam; PF00047; ig; 1.
DR       SMART; SM00406; IGv; 1.
KW       Immunoglobulin V region; Signal.
FT       SIGNAL         1     22
FT       CHAIN         23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT       DOMAIN        23     45       FRAMEWORK 1.
FT       DOMAIN        46     56       COMPLEMENTARITY-DETERMINING 1.
FT       DOMAIN        57     71       FRAMEWORK 2.
FT       DOMAIN        72     78       COMPLEMENTARITY-DETERMINING 2.
FT       DOMAIN        79    110       FRAMEWORK 3.
FT       DOMAIN       111    119       COMPLEMENTARITY-DETERMINING 3.
FT       DOMAIN       120    129       FRAMEWORK 4.
FT       DISULFID      45    110       BY SIMILARITY.
FT       NON_TER      129    129
SQ       SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

Query Match             72.9%;  Score 409.5;  DB 1;  Length 129;
Best Local Similarity   74.8%;  Pred. No.2.6e-36;
Matches    80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
         |||||||||||||||||||||||: :||  ::  |||||||||||:||:|||:|||||
Db   23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS 82
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Qy  61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
        ||||||||||| |||||||||||||||||| |||||| |||||||||
Db  83  RFSGSGSGTDFTLTISSLQPEDSATYYCQQYSTLIITFGQGTRLEIK 129


RESULT 9
ID   KVID_HUMAN          STANDARD;      PRT;   107 AA.
AC   P01596;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;
RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391(1974).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01864; KIHUAR.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   CARBOHYD     28     28       N-LINKED (GLCNAC...).
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11703 MW;  E1BF0DF984C3346 CRC64;

Query Match             72.8%;  Score 409;  DB 1;  Length 107;
Best Local Similarity   68.9%;  Pred. No. 2.4e-36;
Matches   73;  Conservative   20;  Mismatches   13;  Indels   0;  Gaps   0;

Qy   1  DIQMTQSPSSLSASVGDRVTICKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||| ::|||||||||||||||||| |||||||| ||||||||
Db   1  DIQMTQSPSTLSASVGDRVAITCRASQNISSWLAWYQQKPGKAPKVLIYKSSSLESGVPS 60

Qy  61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        ||||||||:|| ||||||||||:||||| |||||| |:|||||:||
Db  61  RFSGSGSGTDFTLTISSLZPBBFATYYCQQYNIFFTFGPGTKVDIK 106


RESULT 10
ID   KV1R_HUMAN          STANDARD;      PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC       AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC       WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A01876; KIHUWE.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Monoclonal antibody.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11840 MW;  9249B61F0945618C CRC64;

Query Match             72.7%;  Score 408.5;  DB 1;  Length 108;
Best Local Similarity   72.0%;  Pred. No. 2.7e-36;
Matches   77;  Conservative   12;  Mismatches   17;  Indels   1;  Gaps   1;

Qy   1  DIQMTQSPSSLSASVGDRVTICKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||| |||||||||||||| ::|||||||||| |||||:|| :|||||||||
Db   1  DIQMTQSPSTLSASVGDRVTITCRASQGIRNDLTWYQQKPGTAPKLIYGATSLQSGVPS 60

Qy  61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||||  || |||||:||||||||| ||||| |||||||||:|
Db  61  RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEVK 107


RESULT 11
ID   KV1H_HUMAN          STANDARD;      PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION HAU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01868; KIHUHU.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
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RESULT 12

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RESULT 12
KVIF_HUMAN

ID   KVIF_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01598;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [2]
RP   SEQUENCE, DISULFIDE BOND.
RX   MEDLINE=71064023; PubMed=4921144;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain.";
RL   Biochemistry 9:3155-3161(1970).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01866; KIHUEU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11788 MW;   9CD294F2F4D88823 CRC64;

SQ   SEQUENCE   108 AA;   11671 MW;   08D3A6160D8D0618 CRC64;

Query Match
Best Local Similarity   71.6%;   Score 402.5;   DB 1;   Length 108;
         Similarity     72.9%;   Pred. No. 1.2e-35;
Matches   78;   Conservative   12;   Mismatches   16;   Indels   1;   Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHTSALQPGIPS 60
          |||||||||||||||||||||||: |:||: |||||||| |||::||| ||| |:||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWTQQKPGKAPQVLIYAASSLPSGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
          |||||||| :|||||||||||: |||||| |  ||:||||||||:|||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTIPTSFGQGTRVEIK 107
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RESULT 13

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RESULT 13
KV1V_HUMAN

ID   KV1V_HUMAN     STANDARD;      PRT;   108 AA.
AC   P04430;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION BAN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86174817; PubMed=3083240;
RA   Dwulet F.E., O'Connor T.P., Benson M.D.;
RT   "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL   Mol. Immunol. 23:73-78(1986).
DR   PIR; A01878; KIHUBN.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Amyloid.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;   11840 MW;   CD3FD944FE96FD37 CRC64;

Query Match
Best Local Similarity   70.7%;   Score 397.5;   DB 1;   Length 108;
         Similarity     70.1%;   Pred. No. 3.9e-35;
Matches   75;   Conservative   16;   Mismatches   15;   Indels   1;   Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHTSALQPGIPS 60
          |||||||||||||||||||||||: |:||: |||||||| |||::||| ||:|| |:||
Db    1 DIQLTQSPSSLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
          ||:|||||| :|||||||||:||||||| |  ||:||||||||:|||
Db   61 RFIGSGSGTEFTLTISSLQPDDFATYYCQQYNSDSKMFGQGTKVEVK 107
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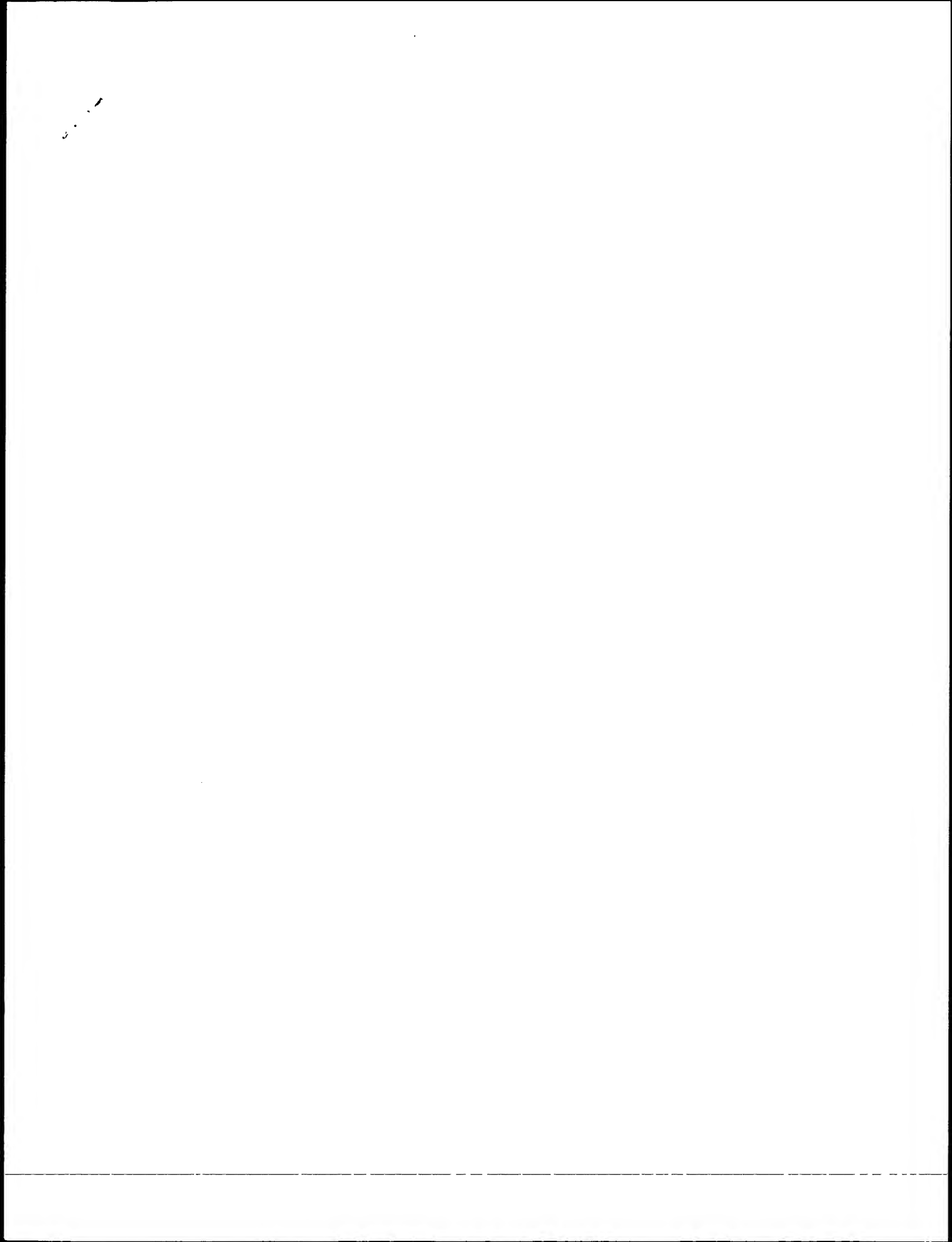
RESULT 14

```
RESULT 14
KV1K_HUMAN

ID   KV1K_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01603;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION KA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76189985; PubMed=818073;
RA   Shinoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

Query Match
Best Local Similarity   70.6%;   Score 396.5;   DB 1;   Length 108;
         Similarity     70.1%;   Pred. No. 5e-35;
Matches   75;   Conservative   14;   Mismatches   17;   Indels   1;   Gaps   1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHTSALQPGIPS 60
          |||||||||||||||||||||||: |:||: |||||||| |||::||| ||:|| |:||
Db    1 DIQLTQSPSSLSASVGDRVTITCRASQSVNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          ||:||||||  |:|||||||||:||||||||||| ||||||||||||
Db   61 NFTGSGSGTDFTLTISSLQPEDFATYYCLQYDNLWTFGQGTKVEIK 106
```

```
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01869; KIHUKA.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11900 MW;  768839FBED5A2F4B CRC64;

Query Match             69.5%;  Score 390.5;  DB 1;  Length 108;
Best Local Similarity   66.4%;  Pred. No. 2.1e-34;
Matches   71;  Conservative 19;  Mismatches 16;  Indels  1;  Gaps  1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              |||||||||||| || |  |: |: |.|:|  |:||   |||||||:|||||||:||
Db          1 DIQMTQSPSTLSVSVGDRVTITCEASQTVLSYLNWYQQKPGKAPKLLIYAASSLETGVPS 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
              |||||||| ||:|||||||||||||||| |:|  ||||||||||:
Db         61 RFSGGQSGTBFTFISSVZZBFATYYCQZILDLPRTFGQGTKVDLK 107
```

```
RESULT 15
ID   KV1E_HUMAN     STANDARD;     PRT;   108 AA.
AC   P01597;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION DEE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72053133; PubMed=5124396;
RA   Milstein C.P., Deverson E.V.;
RT   "The amino acid sequence of a human kappa light chain.";
RL   Biochem. J. 123:945-958(1971).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01865; KIHUDE.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11661 MW;  BDD6E35001F1E51 CRC64;

Query Match             69.18%;  Score 388.5;  DB 1;  Length 108;
Best Local Similarity   68.98%;  Pred. No. 3.4e-34;
```

```
Matches   73;  Conservative  13;  Mismatches  19;  Indels  1;  Gaps  1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              :|:|||||| |||||||||||| :| ||:|   |:||   |||||||:|||||||:||
Db          1 BIZMTQSPSLSASVGDRVTITCRAGQSVNKYLNWYQQKPGKAPKVLIFAASSLKSGVPS 60

Qy         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEI 105
              |||||||| |:| ||| ||| |||||||| |:| |||||||||||:
Db         61 RFSGGSGGTDFTLTIISGLLPEDFATYYCQQSYTTPYTFGPGTKVEM 106

Search completed: May  7, 2002, 12:32:34
Job time: 565 sec
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```
OM protein - protein search, using sw model

                    GenCore version 4.5
                    Copyright (c) 1993 - 2000 Compugen Ltd.

Run on:             May  7, 2002, 12:31:42 ; Search time 67.26 Seconds
                                            (without alignments)
                                            230.521 Million cell updates/sec

Title:              US-09-155-739-7
Perfect score:      562
Sequence:           1 DIQMTQSPSSLSASVGDRVT...........YCLQYDNLWTFGQGTKVEIK 106

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched:           473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters:     473505

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :          SPTREMBL_17:
                    1:  sp_archea:*
                    2:  sp_bacteria:*
                    3:  sp_fungi:*
                    4:  sp_human:*
                    5:  sp_invertebrate:*
                    6:  sp_mammal:*
                    7:  sp_mhc:*
                    8:  sp_organelle:*
                    9:  sp_phage:*
                    10: sp_plant:*
                    11: sp_rodent:*
                    12: sp_virus:*
                    13: sp_vertebrate:*
                    14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

```
                          Query
Result                    Match   Length  DB
No.      Score            Length  DB      ID          Description
------   -----            ------  ------  ----------  -----------
1        428.5    76.2    108     4       Q9UL77      Q9ul77 homo sapien
2        406.5    72.2    108     4       Q9UL70      Q9ul70 homo sapien
3        395      70.3    107     4       Q9UL81      Q9ul81 homo sapien
4        385.5    68.6    108     4       Q9UL79      Q9ul79 homo sapien
5        384.5    68.4    214     11      Q9R1A5      Q9r1a5 mus musculu
6        362.5    64.5    107     11      Q9JL84      Q9jl84 mus musculu
7        337.5    60.1    298     11      Q9QYF0      Q9qyf0 mus musculu
8        336.5    59.9    108     4       Q9UL83      Q9ul83 homo sapien
9        332      59.1    109     4       Q9UL85      Q9ul85 homo sapien
10       331      58.9    109     4       Q9UL78      Q9ul78 homo sapien
11       329      58.5    109     4       Q9UL86      Q9ul86 homo sapien
12       307.5    54.7    107     11      Q9ER29      Q9er29 mus musculu
13       302.5    53.8    99      11      Q9JL74      Q9jl74 mus musculu
14       297      52.8    106     5       Q9U410      Q9u410 schistosoma
15       294      52.3    238     11      Q99M37      Q99m37 mus musculu
16       292.5    52.0    114     4       Q9UL80      Q9ul80 homo sapien
17       284.5    50.6    101     11      Q9JL78      Q9jl78 mus musculu
18       281.5    50.1    97      11      Q9JL76      Q9jl76 mus musculu
19       273.5    48.7    109     6       Q9N0W5      Q9n0w5 oryctolagus
20       269.5    48.0    103     11      Q9JL80      Q9jl80 mus musculu
21       255      45.4    104     11      Q9JL82      Q9jl82 mus musculu
22       212.5    37.8    107     4       Q9UL82      Q9ul82 homo sapien
23       206      36.7    107     4       Q9NSD6      Q9nsd6 homo sapien
24       183      32.6    109     11      Q9ET13      Q9et13 mus musculu
25       170      30.2    130     4       Q9NP29      Q9np29 homo sapien
26       168      29.9    235     11      Q99M11      Q99m11 mus musculu
27       165      29.4    337     13      Q91B02      Q91b02 sphoeroides
28       141.5    25.2    135     4       Q9H5Z4      Q9h5z4 homo sapien
29       141      25.1    342     13      Q1B00       Q91b00 sphoeroides
30       132.5    23.6    93      4       Q9UL76      Q9ul76 homo sapien
31       125      22.2    334     13      Q91B05      Q91b05 sphoeroides
32       124      22.1    123     11      Q61243      Q61243 mus musculu
33       115      20.5    339     13      Q91AY8      Q91ay8 sphoeroides
34       110      19.6    339     13      Q91AZ1      Q91az1 sphoeroides
35       109.5    19.5    118     11      Q91C4       Q92ic4 mus musculu
36       109.5    19.5    169     4       Q9Y2N4      Q9y2n4 homo sapien
37       109      19.4    326     13      Q91AY7      Q91ay7 sphoeroides
38       109      19.4    473     11      Q9D8L4      Q9d8l4 mus musculu
39       108.5    19.3    118     4       Q91B1      Q91b1 homo sapien
40       108      19.2    332     13      Q91B08      Q91b08 sphoeroides
41       108      19.2    339     13      Q91AZ7      Q91az7 sphoeroides
42       107.5    19.1    118     4       Q9UL72      Q9ul72 homo sapien
43       107      19.0    341     13      Q91B06      Q91b06 sphoeroides
44       106      18.9    326     13      Q91AZ5      Q91az5 sphoeroides
45       106      18.9    509     11      Q9X57       Q9x57 mus musculu
```

```
RESULT        1
Q9UL77
ID      Q9UL77;      PRELIMINARY;      PRT;      108 AA.
AC      Q9UL77;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
CC      -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC          DOMAIN.
DR      EMBL; AF035037; AAD56273.1; -.
DR      HSSP; P01607; 1REI.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
FT      NON_TER       1
FT      NON_TER       108
SQ      SEQUENCE      108 AA;  11738 MW;  C06681716C4D16F3 CRC64;

Query Match             76.2%;  Score 428.5;  DB 4;  Length 108;
Best Local Similarity   76.6%;  Pred. No. 3.3e-40;
Matches    82;  Conservative    8;  Mismatches   16;  Indels    1;  Gaps    1;

Qy        1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
              |||||||||||||||||||||||||| ||| ||||||||||| |||:||| ||| |||||
Db        1  DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS  60

Qy       61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK  106
```

```
Db      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSYSWTFGEGTKVEIK 107
           |||||||| |:| |||||||| |||    | |||  |::|:|||||||
```

RESULT 2

ID   Q9UL70   PRELIMINARY;   PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match   72.3%; Score 406.5; DB 4; Length 108;
Best Local Similarity   72.9%; Pred. No. 9.3e-38;
Matches   78; Conservative   12; Mismatches   16; Indels   1; Gaps   1;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||||||||||||:||||||||||||||||||||||||||:|||||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||||| |:|:|||||||:|||  |:|:     |||||||:|||
Db  61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSYSALTFGPGTKLEIK 107
```

RESULT 3

ID   Q9UL81   PRELIMINARY;   PRT;   107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035033; AAD56269.1; -.

Query Match   72.0%; Score 385.5; DB 4; Length 108;
Best Local Similarity   68.6%; Pred. No. 2e-35;
Matches   77; Conservative   8; Mismatches   21; Indels   1; Gaps   1;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||:|:||||||||||||:||:|||| |::|||||||||||||:|||||||
Db   1 DIVMTQSPSSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        ||||||||| |:|  ||||||:|||  | |:     |||||||:|||
Db  61 RFSGSGSGTDFTLTISCLQSEDEFATYYCQQYSFPPTFGQGTKVEIK 107
```

RESULT 4

ID   Q9UL79   PRELIMINARY;   PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11501 MW; 070549FDFD0754748 CRC64;

Query Match   70.3%; Score 395; DB 4; Length 107;
Best Local Similarity   71.7%; Pred. No. 1.7e-36;
Matches   76; Conservative   10; Mismatches   20; Indels   0; Gaps   0;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||||||||||||:||||||||||||||||||||||||||:|||||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        |||||||| |:|:|||||||:||| |:|:     |||||||:|||
Db  61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQYSYSALTFGPGTKVDIR 106
```

DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1
FT   NON_TER   107   107
SQ   SEQUENCE   107 AA; 11787 MW; DB5845F19724FB4E CRC64;

RESULT 5

ID   Q9R1A5
AC   Q9R1A5;   PRELIMINARY;   PRT;   214 AA.

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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFv).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF152371; AAD40242.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     214    214
SQ   SEQUENCE   214 AA;  23922 MW;  52BA205FDE995E2A CRC64;

Query Match             Best Local Similarity    68.4%;
                        Matches     71;  Conservative    18;
Score 384.5; DB 11; Length 214;
Pred. No. 5.7e-35; Mismatches  17;  Indels   1;  Gaps   1;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
         ||||||||||||||| |||||| ::||| ||||       || |||||:|||||||||||
Db    1  DIQLTQSPSSMYASLGERVTICCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK  106
         ||||||||:||: |||| : ||:| ||| |||:    ||| |||:|||
Db   61  RFSGSGSGQDYSLTISSLEYEDMGIYCLQYDEFPTFGSGTKLEIK  107


RESULT 6
ID   Q9JL84     PRELIMINARY;   PRT;   107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Makiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206022; AAF69320.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11648 MW;  ACF9B1253ACA1E5D CRC64;
```

```
RESULT 7
ID   Q9QYF0     PRELIMINARY;   PRT;   298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SCFV.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RA   Shinohara N., Demura T., Fukuda H.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RT   "Isolation of a novel type of vascular cell wall-specific monoclonal
RT   antibody recognizing a cell polarity using a phage display subtraction
RT   method.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA;  31867 MW;  E0F96B8A17004317 CRC64;

Query Match             Best Local Similarity    64.5%;
                        Matches     70;  Conservative    11;
Score 362.5; DB 11; Length 107;
Pred. No. 7.2e-33; Mismatches  25;  Indels   1;  Gaps   1;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
         |||||||| ||||| ||||| :||| |||                 ||||||:||||:|||
Db    1  DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS  60

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK  106
         ||||||||:||||||||||||||||||| |||:    |||:|||||||
Db   61  RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK  107


RESULT 8
ID   Q9UL83     PRELIMINARY;   PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
```

Query Match   Best Local Similarity   60.1%;
                        Matches   63; Conservative   19;
Score 337.5; DB 11; Length 298;
Pred. No. 1.4e-29; Mismatches 24; Indels   1; Gaps   1;

```
Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
         ||:|||||:::|||||||||||||:::        ||||||:||:  |:|||:  :||||
Db  173  DIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS  232

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK  106
         ||||||||  |::|| ::||:|| ::|||:      :|||:|||||||
Db  233  RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK  279
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827139; PubMed=9614934;
RA   Young D.C., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035031; AAD56267.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;

Qy       1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
            : ||||||:|:|| |||||| |:|        :|:||||||||||||:||:||||| ||||
Db       1  EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA  60

Qy      61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK  106
            |||||||| ||||| ::| |||||||| |||||||   ||||||||:|
Db      61  RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK  107

Query Match                    59.9%;
Best Local Similarity   60.2%;
Matches   65;  Conservative   17;  Mismatches   23;  Indels    3;  Gaps    2;

RESULT   9
ID   Q9UL85
AC   Q9UL85;                 PRELIMINARY;       PRT;       109 AA.
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827139; PubMed=9614934;
RA   Young D.C., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035029; AAD56265.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;

Query Match                    59.18%;         Score 332;  DB 4;  Length 109;
Best Local Similarity   61.5%;         Pred. No. 1.8e-29;
```

```
Matches   67;  Conservative   14;  Mismatches   24;  Indels    4;  Gaps    2;

Qy       1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS  60
            : ||||||:|:|| |||||| |:|        :|:||||||||||||:||:||||| ||||
Db       1  EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA  60

Qy      61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK  106
            |||||||| ||||| ::| |||||||| |||||||   ||||||||:|
Db      61  RFSGSGSGTEFTLTISSLQSEDFAIYHCQQY-NSWPPLTFGGGTKVEIK  108

RESULT   10
ID   Q9UL78
AC   Q9UL78;                 PRELIMINARY;       PRT;       109 AA.
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827139; PubMed=9614934;
RA   Young D.C., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035036; AAD56272.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

Query Match                    58.9%;          Score 331;  DB 4;  Length 109;
Best Local Similarity   60.2%;          Pred. No. 2.3e-29;
Matches   65;  Conservative   16;  Mismatches   25;  Indels    2;  Gaps    2;

Qy       1  DIQMTQSPSSLSASVGDRVTITCKTSQDI-NKYMAWYQQTPGKAPRLLIHYTSALQPGIP  59
            : ||||||:|:|| |||||| |:|     : | ||||||||||||||:||:||||| |||
Db       1  EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIP  60

Qy      60  SRFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK  106
            |||||||||| |||| ::| ||| || ||| |  | | |||||||||
Db      61  DRFSGSGSGTDFPLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK  108

RESULT   11
ID   Q9UL86
AC   Q9UL86;                 PRELIMINARY;       PRT;       109 AA.
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9827139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
```

RA   Yeung D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF035028; AAD56264.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1.
FT   NON_TER   109   109.
SQ   SEQUENCE   109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDI-NKYMAWYQQTPGKAPRLLIHYTSALQPGIP 59
         : :||||||| ||:|:|| || :|:||| |:|||||||||| ||:||||||: ||
Db   1 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

Qy   60 SRFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
         |||||||| ||:|| || ||||||:||||| |:|||:|||||||:|
Db   61 DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108

Query Match   58.5%; Score 329; DB 4; Length 109;
Best Local Similarity   58.3%; Pred. No. 3.3e-29;
Matches   63; Conservative   19; Mismatches   24; Indels   2; Gaps   2;

RESULT 13
ID   Q9JL74   PRELIMINARY;   PRT;   99 AA.
AC   Q9JL74;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC   DOMAIN.
DR   EMBL; AF206032; AAF69330.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER   1   1.
FT   NON_TER   99   99.
SQ   SEQUENCE   99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Qy   4 MTQSPSSLSASVGDRVTITCKTSQDI------NKYMAWYQQTPGKAPRLLIHYTSALQPG 57
         |||||||| ||| :|:||| :|:||| :|:||||||||| ||:||||||: ||
Db   1 MTQSPSSLAMSVGQKVTMSCKSSQSQSVLNSNTQKNYLAWYQKPGQSPELIVFAASRESG 60

Qy   58 IPSRFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKV 103
         |:||||||||| ||:|| || ||||||:||||| |:|||:|||||||
Db   61 VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRPFTFGSGTKL 107

Matches   57; Conservative   21; Mismatches   22; Indels   7; Gaps   2;
Query Match   58.8%; Score 307.5; DB 11; Length 99;
Best Local Similarity   58.8%; Pred. No. 3.1e-26;
Matches   57; Conservative   16; Mismatches   23; Indels   1; Gaps   1;

RESULT 14
ID   Q90410   PRELIMINARY;   PRT;   106 AA.
AC   Q90410;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC   Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC   Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the light chain

Qy   11 LSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPSRFSGSGSGRD 70
         |:||||||||||| :|:|| ||||||||| ||:||||||: ||| |:||||||| ||
Db   3 LLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGSGYTD 62

Qy   71 YTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
         |:|| || ||||||:||||| |:|||:|||||||:|
Db   63 FTFTISTVQAEDLAVYFCQQDYSSPRTFGGGTKLEIK 99

Query Match   54.7%; Score 307.5; DB 11; Length 107;
Best Local Similarity   53.3%; Pred. No. 9.3e-27;

```
RT    variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT    Schistosoma japonicum.";
RL    Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC    -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC        DOMAIN.
DR    EMBL; AF207620; AAF19434.1; -.
DR    HSSP; P01679; 2FBJ.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF00047; ig; 1.
DR    SMART; SM00406; IGv; 1.
FT    NON_TER    1        1
FT    NON_TER    106      106
SQ    SEQUENCE   106 AA;  11478 MW;  F20F544426BAE63E CRC64;
```

```
Query Match          52.8%;    Score 297; DB 5;  Length 106;
Best Local Similarity   54.8%;    Pred. No. 1.3e-25;
Matches    57;   Conservative   20;   Mismatches   25;   Indels    2;   Gaps    2;

Qy     4 MTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPSRFS 63
           ||||| :||| ::|||||| |:|||||:|| :|| ||:|||||||||:||||:||:| |||
Db     4 LTQSPAIMSASPGEKVTMTCSASSSVS-YVYWLQKPGSSPRLLIYDTSNLASGVPVRFS 62

Qy    64 GSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          |||||  |:|  |||||| ||||||||| ::  :||| |||:|:|
Db    63 GSGSGTSYSLTISRMEAEDAATYYCQQWTSYPTFGSGTKLELK 106
```

```
RESULT  15
ID   Q99M37
AC   Q99M37;              PRELIMINARY;        PRT;     238 AA.
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:5947).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY TUMOR;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002035; AAH02035.1; -.
SQ   SEQUENCE   238 AA;  26344 MW;  FB2B06A0B801330A CRC64;
```

```
Query Match          52.3%;    Score 294; DB 11;  Length 238;
Best Local Similarity   50.0%;    Pred. No. 7.4e-25;
Matches    56;   Conservative   22;   Mismatches   28;   Indels    6;   Gaps    2;

Qy     1 DIQMTQSPSSLSASVGDRVTITCKTSQDI-----NKYMAWYQQTPGKAPRLLIHYTSALQ 55
           |:||||| || |||| | |:|:|::|||:|         |:||||:|||||||||||:|||:|  |
Db    20 DVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79

Qy    56 PGIPSRFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          || :| ||| |||||| |:| |||:||  ||:|||||| ::  :||| |||:|:|
Db    80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIK 131
```

Search completed: May 7, 2002, 12:31:42
Job time: 628 sec